

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 00:45:14 ; Search time 189 Seconds
(without alignments)
2675.714 Million cell updates/sec

Title: US-09-515-806A-2
Perfect score: 8544
Sequence: 1 MAGGAGPGRGRDEPPESYP.....KKVSVLFYSYRDYRILF 1649

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /cgn2_6/ptodata/2/ina/5B COMB.seq:
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5: /cgn2_6/ptodata/2/ina/6C COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	416	4.9	2628	1	US-08-143-219-1
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6	413.5	4.8	2562	2	US-08-434-998-8
7	413.5	4.8	2562	2	US-08-487-797-8
8	413.5	4.8	2562	5	PCT-US95-02058-8
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10	303.5	3.6	4411529	4	US-09-103-840A-1
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14	284.5	3.3	3089	3	US-08-461-145C-5	Sequence 5, Appli
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16	284.5	3.3	3332	4	US-09-423-890-11	Sequence 11, Appli
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18	282	3.3	3201	3	US-09-340-993-1	Sequence 1, Appli
19	282	3.3	3201	4	US-09-468-442-1	Sequence 1, Appli
20	278.5	3.3	3201	4	US-09-423-890-5	Sequence 5, Appli
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37	263.5	3.1	1353	3	US-09-340-993-8	Sequence 8, Appli
38	263.5	3.1	1353	4	US-09-468-442-8	Sequence 8, Appli
39	263	3.1	3435	4	US-09-046-158A-21	Sequence 21, Appli
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ALIGNMENTS

RESULT 1

US-07-938-782A-1
; Sequence 1, Application US/07938782A
; Patent No. 5525513
; GENERAL INFORMATION:
; APPLICANT: Chen, Jane J.
; APPLICANT: London, Irving M.
; TITLE OF INVENTION: DNA Encoding the Heme-Regulated
; TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha kinase
; NUMBER OF INVENTIONS: 15
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07938,782A
; FILING DATE: 31-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
; TELEFAX: (404)873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

LENGTH: 2729 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rabbit
CELL TYPE: Reticulocytes
FEATURE:
NAME/KEY: misc feature
LOCATION: 113..2149
OTHER INFORMATION: /note= "Expression of HRI
OTHER INFORMATION: mRNA in Human erythroid cells, using as the
OTHER INFORMATION: probe rabbit HRI cDNA from nucleotides 113
OTHER INFORMATION: to 2149."
FEATURE:
NAME/KEY: misc feature
LOCATION: 229..249
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
FEATURE:
NAME/KEY: misc feature
LOCATION: 543..560
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
FEATURE:
NAME/KEY: misc feature
LOCATION: 448..468
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
FEATURE:
NAME/KEY: misc feature
LOCATION: 1009..1031
OTHER INFORMATION: /note= "Primer used in the
OTHER INFORMATION: amplification of a human HRI cDNA sequence
OTHER INFORMATION: using the rabbit HRI cDNA sequence."
PUBLICATION INFORMATION:
AUTHORS: Chen, Jane J.
TITLE: Cloning of the cDNA of the heme-
TITLE: regulated eukaryotic initiation factor
TITLE: 2alpha (eif-2alpha) kinase of rabbit reticulocytes:
TITLE: Homology to yeast GCN2 protein kinase and human
TITLE: double-stranded-RNA-dependent
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 88
PAGES: 7729-7733
DATE: September-1991
US-07-938-782A-1

Alignment Scores:
Pred. No.: 1.48e-38 Length: 2729
Score: 480.50 Matches: 184
Percent Similarity: 43.91% Conservative: 97
Best Local Similarity: 28.75% Mismatches: 241
Query Match: 5.62% Indels: 119
DB: 29 Gaps: 1

US-09-515-806A-2 (1-1649) x US-07-938-782A-1 (1-2729)

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QY 676 Ala-----LysAspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeu 693
DB 890 TCTCACCAGGAAGAGACAGAGATCAATATGGTGTAAATAATGATCAAGCAGCAGCTCA 949
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DB 1166 TCCGCGGAGGAATCTTCTGAGAGAGCTTAAGCGCTTGCGG-----1207
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DB 1208 -----CACACAGAGGTGCAGTACCACCTGATGCTGCATATCCAGATGCAGCTGTC 1258
QY 806 GluLysSer-----ThrLeuArgAspThrIleAsp 815
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QY 816 GlnGlyLeu-----TyrArgAspThrValArgLeuTyrArgLeuPheArgGluIleLeu 833
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QY 834 AspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsn 853
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DB 1541 GAGAGAGACCCACACACACTTCCCGAGGTGGGACCTGCTGTCTAGCTTCCCTCGCCGAGCAG 1600
QY 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
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GENERAL INFORMATION:
APPLICANT: Massachusetts Institute Of Technology
TITLE OF INVENTION: DNA Encoding the Heme-Regulated
TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street

CITY: Atlanta
 STATE: Georgia
 COUNTRY: US
 ZIP: 30309
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08131
 FILING DATE:
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Fabst, Patrea L.
 REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: MIT 5807
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-815-6508
 TELEFAX: 404-815-6555

SEQUENCE FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2729 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Rabbit
 CELL TYPE: Reticulocytes

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 113..2149

OTHER INFORMATION: /note= "Expression of HRI mRNA in Human erythroid cells,"

NAME/KEY: misc_feature
 LOCATION: 229..249

OTHER INFORMATION: /note= "Primer used in the amplification of human HRI cDN

NAME/KEY: misc_feature
 LOCATION: 543..560

OTHER INFORMATION: /note= "Primer used in the amplification of human HRI cDN

NAME/KEY: misc_feature
 LOCATION: 448..468

OTHER INFORMATION: /note= "Primer used in the amplification of human HRI cDN

NAME/KEY: misc_feature
 LOCATION: 1009..1031

OTHER INFORMATION: /note= "Primer used in the amplification of a human HRI c

AUTHORS: Chen, Jane J.
 TITLES: Cloning of the cDNA of the heme-regulated
 TITLE: eukaryotic initiation factor 2alpha
 TITLE: (eif-2alpha)kinase of rabbit reticulocytes:
 TITLE: Homology to yeast GCN2 protein kinase and human
 TITLE: double-stranded-RNA-dependent

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 VOLUME: 88

PAGES: 7729-7733

DATE: September-1991

PCT-US93-08131-1

Alignment Scores:

Pred. No.: 1 48e-38

Score: 480.50

Percent Similarity: 43.91%

Best Local Similarity: 28.75%

Query Match: 241

Indels: 119

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 Db 590 GAAGCAGACAGCTTCAAGTAACTTGAATGAGTTTGAAGAGCTTCCATCTCTGGGAAGGT 649
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 Db 650 GGCTATGGCCGAGTGTACAGAGTTCAGGAATAAATAGATGCCAGTATTATGCAATATAA 709
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 Db 1070 GAGTTTGAATCTCTCAGCGAG-----CGCAAGAGAACGCTCGATCTGGAGCGT 1120
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 QY 788 ProSerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCys 805
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 Db 1439 ATTTTCTTCATGGTCTGATCAACAGTGAATAATAGAGACTTTGGTCTGCGC----- 1492
 QY 873 HisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer 892
 Db 1493 -----TGCGCCGACATCATCCAGAGAATGCGCGCCGACACAGCAAAACGGG 1540
 QY 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911

STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,219
FILING DATE: October 25, 1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION NUMBER: 08/141,244
FILING DATE: October 22, 1993
APPLICATION NUMBER: 07/953,681
FILING DATE: September 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Douglas E. Olson
REGISTRATION NUMBER: 22,798
REFERENCE/DOCKET NUMBER: 204/139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2628 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE: HUMAN PKR GENE, FIGURE 5
INDIVIDUAL ISOLATE:
FEATURE:
NAME/KEY: CDS
LOCATION: 187..1836
US-08-143-219-1

Alignment Scores:
Pred. No.: 5,72e-32 Length: 2628
Score: 416.00 Matches: 179
Percent Similarity: 37.10% Conservative: 87
Best Local Similarity: 24.97% Mismatches: 197
Query Match: 4.87% Indels: 255
Gaps: 31
DB:

US-09-515-806A-2 (1-1649) x US-08-143-219-1 (1-2628)

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Db 475 TCCATGGGGAATTACATAGCGCTTATCAATAGATTGCC-----CAGAGAAAGAACTA 528
QY 406 ThrAla-----GlnLeuLeuSerGlyLeuAspTyrLeuHisSerValVal 422
Db 529 ACTGTAAATTAATGACAGTGTGCATCGGG-----GTGCATGGCCGCAAGGATTT 579

RESULT 4
US-08-143-219-1
Sequence 1, Application US/08143219
Patent No. 5670330
GENERAL INFORMATION:
APPLICANT: Sonenberg, Nahum
APPLICANT: Katze, Michael G.
APPLICANT: Roy, Sophie
APPLICANT: Koromilas, Antonis E.
APPLICANT: Barber, Glen N.
TITLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lvov & Lvov

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QY 423 His----- 423
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QY 424 -----LysValLeuSerAlaSerAsnVal-----LeuValAspAlaGluGlyThr 438
Db 640 GAAGCAAAACAAATGGCGCTAAACTTCATATATCTTCAGATATATCAGAGAAACCTCA 699
QY 439 ValLysIleThrAspTyrSerIleSerLysArgLeuAlaAspIleCysLysGluAspVal 458
Db 700 GTGAAA---TCGACTACTGCTCTCTGGTCTCTTTGCTACTACGTGTGAGTCC----- 750
QY 459 PheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys 478
Db 751 -----CAAAGCAACTCTTTAGTGACCAGACA----- 777
QY 479 GlyAspValTyrArgLeuGlyLeuLeuLeuSerLeuSerGlnGlyGlnGlyCysGly 498
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Db 838 -----AGTGACAGTTTAAACAGTCTCTGTTGCTTATGAATGGTCTC 879
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Db 946 ACAAGATATATCTGCGACAGAGGTTTGGCATGGATTTAAAGAAATAGAATTAATTTGC 1005
QY 598 LysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysTyrAla 617
Db 1006 TCAGTGGATTGGCCAAAGTTTCAAAGCAAAACACAGAATTGACGGAAGACTTACGTT 1065
QY 618 ValLysArgIleProIleAsnProAlaSerArgGlnPheArgIleLysGlyGluVal 637
Db 1066 ATTAACGTGTAAATATAATAAC-----GAGAGCGCGAGCGTGAAGTA 1110
QY 638 ThrLeuLeuSerArgLeuHisGluAsnIleValArgTyrTyrAsnAlaTrpIleGlu 657
Db 1111 AAAGCATTTGGCAAACTTGATCATGTAAATATTGTTCACTACAATGGCTGTGG----- 1164
QY 658 ArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLys 677
Db 1164 ----- 1164
QY 678 AspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeuAspSerValGlu 697
Db 1165 -----GATGATTGAT----- 1176
QY 698 AlaAlaProProIleLeuSerSerValGluTrpSerThrSerGlyGluArg 717
Db 1176 ----- 1176
QY 718 SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspAspGluAspAsp 737
Db 1177 -----TATGATCTGACACCATGATGATCT----- 1203
QY 738 GluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer 757
Db 1204 -----CTTGAGAGCAGT----- 1215

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QY 758 AspIlePheAspAsnGluAspGluAsnSerLysSerGlnAsnGlnAspGluAspCys 777
Db 1216 -----GATTATCATCTGAGAACACGAAAAATAGTTCAAG----- 1251
QY 778 AsnGluLysAsnGlyCysHisGluSerGluProSerValThrThrGluAlaValHisTyr 797
Db 1252 -----TCAAAGACTAAGTGC----- 1266
QY 798 LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp----- 815
Db 1267 CTTTTCATCAAAATGGAATTTCTGTATAAAGGACCTTGGAAACAATGGATTCAAAAAAGA 1326
QY 816 GlnGlyLeuTyrArgAspThrValArgLeuTyrArgLeuPheArgGluIleLeuAspGly 835
Db 1327 AGAGGCGAGAACTAGACAAAGTTTTGGCTTTGGAACTCTTTTGAACAATAACAAGGG 1386
QY 836 LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePhe 855
Db 1387 GTGGATTATATACATTCAAAAAATAATTATTCATAGATCTTAAGCCAAAGTATATATTC 1446
QY 856 LeuAspSerAspHisValLysIleGlyAspPheGlyLeuAlaThrAspHisLeuAla 875
Db 1447 TTAGTAGATACAAAAACAAGTAAAGATTGGAGACTTTGGACTTTGTAACTCT----- 1497
QY 876 PheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSerAspProSer 895
Db 1498 -----CTGAAAATGAT----- 1509
QY 896 GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer 915
Db 1510 GGAAGCGCAACAAGAGTAAGGAACTTTGGCATACATGAGCCAGAACAGATTCTTCG 1569
QY 916 ThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIleIlePhePheGlu 935
Db 1570 -----CAAGACTATGGAAGGAACTGAGCTCTACGCTTTGGGCTAATTTCTGCTGAA 1623
QY 936 MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg 955
Db 1624 CTT---CTTCATGTATGTGACACTGCTTTGAAACATCAAAAGTTTTCACAGACCTACGG 1680
QY 956 AspProThrSerProLysPheProGluAspPheAspAspGlyGluHisAlaLysGlnLys 975
Db 1681 GATGCGATC-----ATCTCAGATATATTGAT-----AAAAAGAAAAA 1719
QY 976 SerValIleSerTrpLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995
Db 1720 ACTCTTCACGAAATTAATCTCTCAAAGAAACCTGAGGATCGACCTAACACATCTCTGAAATA 1779
QY 996 LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis 1012
Db 1780 CTAAGGACCTTGACTGTGTGGAAGAAAGCCAGAGAAAAATGAACGACAC 1830

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RESULT 5

US-08-436-771-8

; Sequence 8, Application US/08436771

; Patent No. 5861300

; GENERAL INFORMATION:

; APPLICANT: Silverman, Robert H.

; APPLICANT: SenGupta, Dibendu N.

; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &

; ADDRESSEE: Russell

; STREET: 200 E. Broward Boulevard

; CITY: Fort Lauderdale

; STATE: Florida

; COUNTRY: USA

; ZIP: 33301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

Thu Jun 12 14:34:04 2003

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1627 CTT---CTTCATCTATGTGACACTGCTTTTGAACACATCAAAAGTCTTTTCACAGACCTACGG 1683
956 AspProThrSerProLysPheProGluAspPheAspGlyGluHisAlaLysGlnLys 975
1684 GATGGCATC-----ATCTCAGATATATTGAT-----AAAAAGAAAAA 1722
976 SerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995
1723 ACTCTTCTACAGAAATTTACTCTCAAGAAACCTTGAGGATCGACCTAACACATCTGAAATA 1782
996 LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis 1012
1783 CTAAGGACCTTGTGACTGTGTGGAAGAAAGCCAGAGAAAATAATGACGACAC 1833

RESULT 7
US-08-487-797-8
; Sequence 8, Application US/08487797
; Patent No. 5866787
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: SenGupta, Dibyendu N.
; TITLE OF INVENTION: Transgenic Plants Co-Expressing A
; TITLE OF INVENTION: Functional Human 2-5A System
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Holland & Knight
; STREET: One E. Broward Boulevard, #1300
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,797
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16(C)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/468-7811
; TELEFAX: 305/463-2030
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2562 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-487-797-8

Alignment Scores:
Pred. No.: 9,85e-32 Length: 2562
Score: 413.50 Matches: 179
Percent Similarity: 37.10% Conservative: 87
Best Local Similarity: 24.94% Mismatches: 198
Query Match: 4.84% Indels: 254
Gaps: 31
Db: 2

US-09-515-806A-2 (1-1649) x US-08-487-797-8 (1-2562)
QY 329 GluLysGluLysIleAspLysCysLysLysGlnIleGlnGlyThrGluThrGluPheAsn 348
Db 344 CAGAAAGGTGAAGGTAGATCAAGAGGAAGGACCA----- 376
QY 349 SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys 367
Db 377 -----AAATGCCGACGCAAAATTAGCTGTGTGAGATACTTAAAGGAAAAAGAGG 427

```


CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
 ADDRESSEE: Russell
 STREET: 200 E. Broward Boulevard
 CITY: Fort Lauderdale
 STATE: Florida
 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/02058
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/198,973
 FILING DATE: 18-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: CL11363-16
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305/527/2498
 TELEFAX: 305/764/4996
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2562 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 PCT-US95-02058-8

Alignment Scores:
 Pred. No.: 9.85e-32 Length: 2562
 Score: 413.50 Matches: 179
 Percent Similarity: 37.10% Conservative: 87
 Best Local Similarity: 24.97% Mismatches: 198
 Query Match: 4.84% Indels: 254
 DB: 5 Gaps: 31

US-09-515-806A-2 (1-1649) x PCT-US95-02058-8 (1-2562)

QY	439	VallysileThrAspTyrSerileSerLysArgLeuAlaAspileCysLysGluAspVal	458
Db	700	GTGAAA---TCTGACTACCTGCTCTGTTCTTTTGTCTACTACGTGTGAGTCC	750
QY	459	PheGluGlnThrArgValArgPheSerAspAlaLeuProTyrLysThrGlyLysLys	478
Db	751	-----CAAAGCAACTCTTTTGTGACACGACCA	777
QY	479	GlyAspValTrpArgLeuGluLeuSerLeuSerGlnGlyGlnGluCysGly	498
Db	778	-----CTCGCTTCTGANTCATCATCTGAAGGT	804
QY	499	GluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLysLys	518
Db	805	-----GACTTCTCAGCAGATACATCAGAGATA	831
QY	519	CysValCysLeuAspAspLysGluAArgTrpSerProGlnGlnLeuLeuLysHisSerPhe	538
Db	832	-----AATTCTAACAGTGACAGTTTAAACAGAGTCTTCGTGTGCTTATGATGCTC	882
QY	539	IleAsnProGlnProLysMetProLeuValGluGlnSerProGluAspSerGlyGln	558
Db	883	AGAAATTAATCAAGGAGGCAAAA	906
QY	559	AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPhePheSerGlu	578
Db	907	-----AGATCTTTGGCACCAGATTTGACCTTCCTGCAC	948
QY	579	ThrGlnArgGlnPheSerArgTyrPhe---IleGluPheGluGluLeuGlnLeuLeuGly	597
Db	949	ACAAAGTATCTGTGGACAGAGGTTTGGCATGATTTAAAGAAATAGAAATTAATTGGC	1008
QY	598	LysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysTyrAla	617
Db	1009	TCAGGTGGATTTGGCCAAAGTTTCAAAGCAAAACACAGAAATTCGCGAAGACTTACGT	1068
QY	618	VallysArgIleProIleAsnProAlaSerArgGlnPheArgGlnLysGlyGluVal	637
Db	1069	ATTAAACGTGTTAAATATAATTAAC	1113
QY	638	ThrLeuLeuSerArgLeuHisGlnAsnIleValArgTyrTyrAsnAlaTrrIleGlu	657
Db	1114	AAAGCATTTGGCAAAACITTCATGATAATATTTCTACATAATGGCTGTGG	1167
QY	658	ArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLys	677
Db	1167	-----	1167
QY	678	AspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeuAspSerValGlu	697
Db	1168	-----GATGATTGTAT	1179
QY	698	AlaAlaAlaProProIleLeuSerSerSerValGluTrpSerThrSerGlyGluArg	717
Db	1179	-----	1179
QY	718	SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspGluAspAsp	737
Db	1180	-----TATGATCTGACACAGTATGATCT	1206
QY	738	GluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer	757
Db	1207	-----CTTGAGAGCAGT	1218
QY	758	AspIleIlePheAspAsnGluAspGluAsnSerLysSerGlnAsnGlnAspGluAspCys	777
Db	1219	-----GATTATGATCTGAGAACAGCAAAATAGTTCAAGG	1254
QY	778	AsnGluLysAsnGlyCysHisGluSerGluProSerValThrGluAlaValHisTyr	797
Db	1255	-----TCAAAGACTAAGTGC	1269

QY	329	GluLysGluLysIleAspLysCysLysGlnIleGlnGlyThrGluThrGluPheAsn	348
Db	344	CAGAAGGTGAAGGTAGATCAAGAGGAGGAGCA	376
QY	349	SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys	367
Db	377	-----AAATGCCCGCAGCCAAATAGCTGTGAGATCTTAAATAGGAAAGAGG	427
QY	368	GluGlnAspAspSerIleValValAspIleLeuValGluHisIleSer	385
Db	428	-----TTAGTCTTTA-TTATTGACAAACAGAAATCTTCAGAGGATTA	474
QY	386	SerLeuAlaAlaHisSerHisSerGlyProIleProValHisGlnLeuArgArgTyr	405
Db	475	TCCATGGGAATTACATAGGCTTATCAATAGATTTGCC	528
QY	406	ThrAla-----GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal	422
Db	529	ACTGTAAATTTAAGACAGTGTGCATCGGG	579
QY	423	His-----	423
Db	580	CATTATAAATGCAAAATGGCAGAGAAATATAGTATTGTTACAGGTTCTACTAAACAG	639
QY	424	-----LysValLeuSerAsnVal-----LeuValAspAlaGluGlyThr	438
Db	640	GAAGCAAAACATTTGCCCTAAACTTGCATATCTTTCAGATATTATCAGAGAAACCTCA	699

Percent Similarity: 36.43% Conservative: 149
 Best Local Similarity: 21.05% Mismatches: 378
 Query Match: 3.55% Indels: 240
 DB: 4 Gaps: 42

US-09-515-806A-2 (1-1649) x US-09-103-840A-2 (1-4403765)

QY	170	GlnGluGlnArgGluLeuLeuHisGluLeuGlnArgArgGluGlu-----lleLys	187
Db	19079	CAGAGCGCGCGGTGTCCAGCGAGTCCGCGTAAGTAACAGAGCTGATGTCGCG	19020
QY	188	GluGluLysLysArgLysGluMetAlaLysGlnGluArgLeuGluLeuAlaSer---	206
Db	19019	GCCGAGAAATCGCAGACGAAAGGGCAATCCCGCGTCGAGATCGATCCCAAGACG	18960
QY	207	SerAsnGlnAspHisThrSerLysLysAspProGlyGlyHisArgThrAlaAlaLeu	226
Db	18959	GGCACC GCCGCAATCGCACCC-----GACCCTCG-TCACACTCCACCGCAGCTTGTA	18907
QY	227	His-----GlyGlySerProAspPheValGlyAsnGly	237
Db	18906	CATCGCCTTTCGCCCGCCGACAGCGCCCAAGTGGCTGT-----TGCCGTCTCGT	18856
QY	238	LysHisArgAlaAsnSerSerGlyArgSerArgGluArgGlnTySerValCys---	256
Db	18855	GGAGAACGGGGCTGATCGCTGTCGCCACCGGAG-----TGCCCT	18814
QY	257	AsnSerGluAspSerProGlySerCysGluLeuLeuTyrPheAsnMetGlySerProAsp	276
Db	18913	CGCGGACCGCATCGCGCGCGGTGATCGA-----AGCGCACTGCAGGGGA	18766
QY	277	GlnLeuMetValHisLysGlyLysCysIleGlySerAspGluGlnLeuGlyLysLeuVal	296
Db	18765	ACCATGAGCCCCGAGTTGGCGTGTCGCGCATACCGCTCCAGCGCTCATC	18706
QY	297	TyrAsnAlaLeuGluThrAlaThrGlyGlyPheValLeuLeuTyrGluTrpValLeuGln	316
Db	18705	-----GCCACCGGTGTATGGGCCAAGTCTGGAGGCCGTG-----	18670
QY	317	TrpGlnLysLysMetGlyProPheLeuThrSerGlnGlu---LysGluLysIleAspLys	335
Db	18669	---GATAACGGTGGCGCGCGTTCGGGTGAAGGTGCTCAAGAGCGATTTCTCTCC	18613
QY	336	CysLysLysGlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHis	355
Db	18612	GATCGGAGTTTCATCGAACGGTTCGGGCCGAGCGCACCCGCGATGCTGAACCAT	18553
QY	356	ProAsnValValArgTyrLeuAlaMetAsnLeuLysGluGlnAsp---AspSerIleVal	374
Db	18552	CGCGCATCGCCAGCGTCAGACTACGCGGAAAGCCAGATGAACGGGAGGGTCGCAGC	18493
QY	375	ValAspIleLeuValGluHisIleSerGlyValSerLeuAlaAlaHisLeuSerHisSer	394
Db	18492	GCCTACCTGGTGATGAGCTGTTCAACGGCGAGCCACTAAATTCGGTGCTCAACGCACC	18433
QY	395	GlyProIleProValHisGlnLeuArgTyrThrAlaGlnLeuLeuSerGlyLeuAsp	414
Db	18432	GGCCGCTGTGTTGGCGCACGCACTGTCGAGCAGACCGCGCGCTCTGCAG	18373
QY	415	TyrLeuHisSerAsnSerValValHisLysValLeuSerAlaSerAsnValValAsp	434
Db	18372	ATCGGCATCGCGCTGGCTGTGCACCGGACGTCAACCGGGCAACATCTTGATCACC	18313
QY	435	AlaGluGlyThrValLysIleThrAspTyrSerIleSerLysArgLeu-----AlaAsp	452
Db	18312	CCCACCGGGCAGGTCAAGATCACGACTTCGGCATGCCAAAGCCGTCGATGCAGCGCC	18253
QY	453	IleCysLysGluAspValPheGluGlnThrArgValArgPheSer---AspAsnAlaLeu	471
Db	18252	GTGACCCAGCCGCATGGTGATGGGCACCGCCCAATACATCCGCGGGAGAGGCCCTC	18193
QY	472	ProTyrLysThrGlyLysLysGlyAspValTrpArgLeuGlyLeuLeuLeuSerLeu	491

Alignment Scores:
Pred. No.: 1.81e-14 Length: 4403765
Score: 303.50 Matches: 204


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; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 1.82e-14 Length: 4411529
Score: 303.50 Matches: 204
Percent Similarity: 36.43% Conservative: 149
Best Local Similarity: 21.05% Mismatches: 378
Query Match: 3.55% Indels: 240
DB: 4 Gaps: 42

US-09-515-806A-2 (1-1649) x US-09-103-840A-1 (1-4411529)

QY 170 GlnGluGlnArgGluLeuLeuHisGluLeuGlnArgArgGluGlu-----IleLys 187
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19079 CAGCAGCGCGCGGGTGTACCGCAGGTGCGCGCTAAGCTAACAGAGCTATGTCGCG 19020

QY 188 GlnGluLysArgLysGluMetAlaLysGlnGluArgLeuGluLeuAlaSer---Leu 206
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19019 GCCGAGAAATGCACACAGAGAAAGGGCAATCCCGCGCTGCATCGATCGATCCAAAGACG 18960

QY 207 SerAsnGlnAspHisThrSerLysLysAspProGlyGlyHisArgThrAlaAlaLeu 226
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19059 GGCACCGCGCAATCGACAC---GACCCCTCG-TCACATCCACCGCAGCTTGTA 18907

QY 227 His-----GlyGlySerProAspPheValGlyAsnGly 237
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18906 CATCGCTTTGGCGCGCACAGCGCCCAAGTGGCTGT-----TGCGGTGCTGT 18856

QY 238 LysHisArgAlaAsnSerSerGlyArgSerArgGluArgGlnTyrSerValCys--- 256
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18855 GGAGAACGGGGTGTATCGCTGTCGCCACCGGAG-----TGCCCT 18814

QY 257 AsnSerGluAspSerProGlySerCysGluLeuLeuTyrPheAsnMetGlySerProAsp 276
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18813 CGCGCACCGATCGGGCGCGCGTATCGA-----AGCCGCACTGCAGGGGGA 18766

QY 277 GlnLeuMetValHisLysGlyLysCysIleGlySerAspGluGlnLeuGlyLysLeuVal 296
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18765 ACCATGAGCCCCGAGTTGGCTGACGCTGCGGCGACATACCGCTGCGACGCCCTCATC 18706

QY 297 TyrAsnAlaLeuGluThrAlaThrGlyPheValLeuLeuTyrGluTrpValLeuGln 316
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18705 -----GCCACCGGTGGTATGGGCCAAGTCTGGAGGCGGTG----- 18670

QY 317 TrpGlnLysLysMetGlyProPheLeuThrSerGlnGlu---LysGluLysIleAspLys 335
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18669 ---GATAACCGTTGGCGCGCGGTGCGGTGAGGTGCTCAGAGCGAGTTCTCCTCC 18613

QY 336 CysLysLysGlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHis 355
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18612 GATCGGAGTTTCAGAACCGGTTCGCGGCCAAGCGCGCACCGCGATGCTGAACCAT 18553

QY 356 ProAsnValValArgTyrLeuAlaMetAsnLeuLysGluGlnAsp---AspSerIleVal 374
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18552 CGCGGCATCGCCCGTCGACGACTACCGGCAAGCGCAGATGAACCGGGAGGTGCGCAG 18493

QY 375 ValAspLeuValGluHisIleSerGlyValSerLeuAlaHisLeuSerHisSer 394
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18492 GCCTACCTGTGTGAGTGTGTCAGCGGCGAGCCCAATTAATCGGTGCTCAACGCGACC 18433

QY 395 GlyProIleProValHisGlnLeuArgTyrThrAlaGlnLeuSerGlyLeuAsp 414
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18432 GCGCGGTGCTGTGCGGACCGCAGCTGACATGCTCGACAGACCGCGCGCTCTGCGAG 18373

QY 415 TyrLeuHisSerAsnSerValValHisLysValLeuSerAlaSerAsnValLeuValAsp 434
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18372 ATCGCGCATCGCGCTGCTGTGTCACCGCGAGCTCAACCGGCAACATCTTGATCACC 18313

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QY 435 AlaGluGlyThrValLysIleThrAspTyrSerIleSerLysArgLeu-----AlaAsp 452
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18312 CCCACCGGCGAGTGAAGATCACCGACTTCGGCATCGCAGACCGCTCATCAGCGGCC 18253

QY 453 IleCysLysGluAspValPheGluGlnThrArgValArgPheSer---AspAsnAlaLeu 471
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18252 GTGACCCAGACCGCGCATGGTGATGGGCACCGCCCAATACATCATCGCGGAGCGCCCTC 18193

QY 472 ProTyrLysThrGlyLysGlyAspValTrpArgLeuGlyLeuLeuLeuSerLeu 491
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18192 GGTACAGACCGCAGCCCGCGCGACGCTATTCTCTGGGAGTTGTTGGGTATGAAGCG 18133

QY 492 SerGlnGly-----GlnGluCys 497
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18132 GTTTCGGGTAAACCGCGGTTCGCGCGGATGGTCCCTGACCGTGGCAATGAAGCACATC 18073

QY 498 GlyGluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeu-Ly 517
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18072 AAGGACCGCGCGCGCTGCTCCCGACCTGCGCCCAATGTCGAGAACTCATCGAG 18013

QY 517 s-----LysCys---ValCysLeuAspLysGlu---Ar 527
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
18012 ATAACCTCTGGTGAAGAACCCCGCGATGCTATCGAGTGGGGACCGTTTCGCGACGCG 17953

QY 527 gTTP-----SerProGlnGlnLeuLeuLysHisSerPheIleAs 540
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17952 GTGGCAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17893

QY 540 nProGlnProLysMetProLeu-ValGluGlnSerProGluAspSerGlyGlyGlnAsp 560
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17892 CGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17833

QY 560 yrValGluThrValIleProSer-----AsnArgLeuProSerAlaAlap 575
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17832 GGCGGACTGCGCGCATCCGTCGATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17774

QY 575 hePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGluPheGluGlnLeu 595
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17773 -----GCGCACGTTTTCGTCCGG---TCAGCGTGGCGCTG 17743

QY 595 euLeuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysc 615
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17742 CTCTGGCGCGCGCGGTGCTGGCGG---TCAGCGTGGCGCTG 17717

QY 615 ysTyrAlaValLysArgIleProIleAsnProAlaSerArgGlnPheArgIleLysG 635
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17717 ----- 17717

QY 635 lyGluValThrLeuLeuSerArgLeuHisGluAsnIleValArgTyrTyrAsnAla 655
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17716 -----GCTGGCAATCATCGCGCTGCTGCTCATCAAGCGCGC- 17675

QY 655 rPleGluArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProL 675
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17674 -----CGGGACCAACAGCGCGCGACGA---GGCAGCGCGCGC- 17642

QY 675 euAlaLysAspAspArg-AlaAlaArgGlyGln---ProAlaSerAspThrAspGlyLeu 693
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17641 -----GACCGTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 17593

QY 694 AspSerValGluAlaAlaProProIleLeuSerSerValGluTrpSerThr 713
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17592 GATGCT-----AGCCCGCGCTCAATGGACGGA 17563

QY 714 SerGlyGlu----- 716
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17562 CGCGGGGAACAGCTATTCTCGACTGCAAGCTGGTGTTCGCGCGCGCGCGCGCGCGCG 17503

QY 717 ArgSerAlaSerAlaArgPheProAlaThrGly-----ProGlySerSerAsp 732
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17502 CGCGCGTCTGCGCGCGCGATACGAGATACCGCAATGACACCGCTTCCAC-CTGTCGAC 17444

QY 733 AspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSerPheLeuPro--- 751

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Qy	436	luGlyThrValIyfeIThrAspYrSerIlleSerLysArgLeuAlaAspIleCysIysG	456
Db	1898	CTGGGAATGTGAAGCTTGGGATTTGGGGCCAGCAACCGCTTACAGCATCTGC	1953
Qy	456	luAspValPheGluClnThrArgValArgPheSerAspAsnAlaLeuProTyr	473
Db	1954	-----ATGTCAGGCAGACGCAATTCGC--TCTGTCACTGGCACACCCCTACTGGATGA	2002
Qy	474	-----LysThrGlyLysLysGlyAspValTrpArgLeuGlyL	486
Db	2003	GTCTGAAGTCATCAGTGGCGAGGGCTATGGAAGAAGCGACACGTTGGAGCTGGCT	2062
Qy	486	euleuLeuLeuSer---LeuSerGlnGlyGlnGluCysGlyGluTyrProVal	502
Db	2063	GTACTGTGGTGGAAATGCTGCACAGAGAAACCACTTGGGCAGAGTATGAAGCTATGGCTG	2122
Qy	503	-----ThrIleProSerAspLeuProAla	511
Db	2123	CCATTTTCAAGATTGCCACCCAGCTTACCAATCTCAGCTGGCTCTCATCTCAGAAC	2182
Qy	511	spPheGlnAspPheLeuLysLysCysValCysLeuAspAspLysGluArgTpsSerProG	531
Db	2183	ACGGCAGGAGACTTCTTGAGGCGC--ATATTTGTGGAACCTCGTCAGAGACCTCAGCTG	2239
Qy	531	lnGlnLeuLeuLysHisSerPhe	538
Db	2240	AGGAGCTGCTCACACACCACTTT	2262
RESULT 12			
US-08-323-460A-5			
; Sequence 5, Application US/08323460A			
; Patent No. 5854043			
; GENERAL INFORMATION:			
; APPLICANT: JOHNSON, GARY L.			
; TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL			
; TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS			
; NUMBER OF SEQUENCES: 10			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH			
; STREET: 1700 LINCOLN STREET, SUITE 3500			
; CITY: DENVER			
; STATE: CO			
; COUNTRY: USA			
; ZIP: 80203			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/323,460A			
; FILING DATE: 14-OCT-1994			
; CLASSIFICATION: 530			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/049,254			
; FILING DATE: 14-APR-1993			
; ATTORNEY/AGENT INFORMATION:			
; NAME: KOVARIK, JOSEPH E.			
; REGISTRATION NUMBER: 33,005			
; REFERENCE/DOCKET NUMBER: 2879-1-1			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 303/863-9700			
; TELEFAX: 303/863-0223			
; INFORMATION FOR SEQ ID NO: 5:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 3089 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: DNA (genomic)			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 400..2280			

Thu Jun 12 14:34:04 2003

US-08-323-460A-5

Alignment Scores:

Pred. No.: 2,38e-18 Length: 3089
Score: 284.50 Matches: 125
Percent Similarity: 39.8% Conservatives: 86
Best Local Similarity: 23.63% Mismatches: 211
Query Match: 3.33% Indels: 107
Gaps: 20

US-09-515-806A-2 (1-1649) x US-08-323-460A-5 (1-3089)

QY 77 valLysCysProProThrTyrProAspValValProGluLleGlu-----LeuLys 93
Db 800 CTGGAGTTCAGGAGGTCGGATCAAGCCCTCCAGCTCGCAGGGGATATAATACCA 859
QY 94 AsnAlaLysGlyLeuSerAsnGluSerValAsnLeuLeuLysSerArgLeuGluLeu 113
Db 860 TCTACCAAGCTCTGAGCCGAGAGCCAGCCACCTCTCTGTCA-----901
QY 114 AlaLysLysHisCysGlyGluValMetIlePheGluLeuAlaTyrHisValGlnSerPhe 133
Db 902 GCTCCCAAGAACCTGGCCGAGCTCTCTCCCTCCCGG-----GATATGTAC 946
QY 134 LeuSerGluHisAsnLysProProLysSerPheHisGluGluMetLeuGluLysGAr 153
Db 947 CTGAGCGACAACAGCACATTCGCGGAGGATCTTATACGAGCATCAACAGCGAGGTG 1006
QY 153 gAlaGlnGluGlnArgLeuLeuGluLys-----ArgLysG1 168
Db 1007 AATTATCTCCAGAGCAGGAGCAAGCTGTATGTAGATCCCTCAGCAGCTGCGGAAAT 1066
QY 168 uGluGlnGluArgGluLeuHisGlnArgArg-LysGluGluLleLysG 188
Db 1067 CTTGTGAGGAGTGCATCTTGGACAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1126
QY 188 luGluLysArgLysGluMetAlaLysGlnGluArgLeuGluLleAlaSerLeuSerA 208
Db 1127 CACAAATGTCGCGAGCGGAGTCTCCAGACAACAGAGGAGTCTCAGATCGGAGA 1186
QY 208 snGlnAspHisThrSerLysLysAspProGlyGly-----HisArgThrAlaAlaI 225
Db 1187 CCCAGCTCTAT---GATAAAGGTGCAAGGTGGAAGCTATCCAGCGCGTACCATGTGT 1243
QY 225 leuHisGlyCysSerProAspPheValGlyAsnGlyLysHisArgAlaAsnSerSerG 245
Db 1244 CTGTGCAT-----CACAAAGACTACAATGATG 1270
QY 245 lyArgSerArg-----ArgGluArgGlnTyrSerValCysAsnSerGluAspS 261
Db 1271 GCAGAGAACATTTCCCGAATACGAGCGCATCAAGCAACCTATTCACTCTGTGCGCCT 1330
QY 261 exProGlySerCysGluLleLeuTyrPheAsnMetGlySerProAspGlnLeuMetValH 281
Db 1331 CAAATGCTCTTGTAGACAAATGCGGAGCAATGGGTGTAGCTGTGCAATACCTGAGC 1390
QY 281 isLysGlyLysCysLleGlySerAspGluGln-----291
Db 1391 CCCGTGGCGCCTACGAGGTGAGAGCTGAGATGAGATGCGCTCACTGTGCGAGAAAGGATG 1450
QY 292 -----LeuGlyLysLeuValTyrAsnA 299
Db 1451 TGCCAAACCAATCTCTAGTGTCTCCATCAATTTGGCGTGGGGAGGCTCTCTG 1503
QY 299 laLeuGluThrAlaThrGlyGlyPheValLeuLeuTyrGluTrpValLeuGlnTrpGlnL 319
Db 1504 -----GTCAAGGTGCTTCGCGAGGCTCTAC-----TTGTGCTATGATG 1543
QY 319 ysLysMetGlyProPheThrSerGlnGlyLysGlu-----lysIleAspLysC 336
Db 1544 TGGACACAGGACGCTGAACTTGTCTTCAAGCAGGTGCGATTTGACCCAGATAGTCTCTGAGA 1603
QY 336 ysLysLysGlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHisP 356

Db 1604 CAAGCAAGGAGGTGAGTGTCTCTGAGTGTGAGATCCAGTTCAGTGAAGAACTTCAGCATG 1663
QY 356 roAsnValValArgTyrLeuAlaMetAsnLeuLysGluGlnAspSerLeuValVala 376
Db 1664 AGCGCATTTGTGAGTACTACGGTGC---CTGGGAGCGTGTCTGAGAAGATCTCTCACC- 1719
QY 376 spLleLeuValGluHisIleSerGlyValSerLeuAlaHisLeuSerHisSerGlyP 396
Db 1720 --ATCTTTATGAGTATATCCAGGGGCTCTCTAAAGACACAGTTCAGAGGCTACGGAG 1777
QY 396 rolleProValHisGlnLeuArgTyrThrAlaGlnLeuLeuSerGlyLeuAspTyrL 416
Db 1778 CTCTGACAGAGGTGTACCCGCAAGTACACCCGCGAGATTCCTGGAGGCGATGTCTATAC 1837
QY 416 euHisSerAsnSerValValHisLysValLeuSerAlaSerAsnValLeuValAspAla 436
Db 1838 TGCACAGCAACATGATGTGTGATCGGAGCATCAAGGAGGCAATATCTCTCCGAGACTCAG 1897
QY 436 luGlyThrValLysIleThrAspTyrSerIleSerLysArgLeuAlaAspIleCysLysG 456
Db 1898 CTGGGAATGTGAAGCTTGGGATTTGGGGCCAGCAAAACGCTACAGACCATCTGC--- 1953
QY 456 luAspValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyr----- 473
Db 1954 -----ATGTACGAGGACAGGCAATTCG---TCTGTCACTGGCACACCTTACTGGATGA 2002
QY 474 -----LysThrGlyLysLysGlyAspValTrpArgLeuGlyL 486
Db 2003 GTTCCTCAACTCATCAGTGGCGAGGCTATGGAAGAAAGGAGGAGCTGTGGAGCCTGGGCT 2062
QY 486 euLeuLeuLeuSer---LeuSerGlnGlyGlnGluCysGlyGlyLysProVal----- 502
Db 2063 GTACTGTGTGGAATGTCTGACAGAGAAACACCTTGGGAGAGTATGAAGCTATGGCTG 2122
QY 503 -----ThrIleProSerAspLeuProAlaA 511
Db 2123 CCATTTCAAGATTGCCACCCAGCTACCAATCTCTCAGTGCCTCTCCATCTCAGAAC 2182
QY 511 spPheGlnAspPheLeuLysLysCysValCysLeuAspAspLysGluArgTrpSerProG 531
Db 2183 ACGGAGGAGTCTCTCTGAGGCGC---ATATTTGTGGAAGCTCTCTCAGAGACCTCAGCTG 2239
QY 531 lngLlnLeuLysHisSerPhe 538
Db 2240 AGGAGTGTCTCACACACCATTT 2262

RESULT 13

US-08-461-146C-5
Sequence 5, Application US/08461146C
Patent No. 5981265
GENERAL INFORMATION:
APPLICANT: JOHNSON, GARY L.
TITLE OF INVENTION: METHODS FOR REGULATING MEKK PROTEIN ACTIVITY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive and Cockfield
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,146C
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/354,516

FILING DATE: 21-FEB-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/049,254
 FILING DATE: 15-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/323,460
 FILING DATE: 14-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/11690
 FILING DATE: 14-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04178
 FILING DATE: 15-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: KARA, Catherine J.
 REGISTRATION NUMBER: P41,106
 REFERENCE/DOCKET NUMBER: CPI-004CN3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3089 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 400..2280
 US-08-461-146C-5

Alignment Scores:
 Pred. No.: 2,38e-18 Length: 3089
 Score: 284.50 Matches: 125
 Percent Similarity: 39.89% Conservative: 86
 Best Local Similarity: 23.63% Mismatches: 211
 Query Match: 3.33% Indels: 107
 DB: 2 Gaps: 20

US-09-515-806A-2 (1-1649) x US-08-461-146C-5 (1-3089)

QY 77 ValLysCysProThrTyrrProAspValValProGluLeuGlu-----LeuLys 93
 Db 800 CTGGAGTCTCCAGCAGGTCGGATCAAGCTTCCAGTCTCCAGTCTGAGGGGATATAATACCA 859
 QY 94 AsnAlaLysGlyLeuSerAsnGluSerValAsnLeuLysSerArgLeuGluLeu 113
 Db 860 TCTACCAAGCTCTTGAGCCAGAGCAGGAGCAGCCTGTCTGTCA----- 901
 QY 114 AlaLysLysHisCysGlyGluValMetIlePheGluLeuAlaTyrrHisValGlnSerPhe 133
 Db 902 GCTCCAGAACCTTGGCCGAGGCTCTCTCCCTCCCGG-----GATATGTATC 946
 QY 134 LeuSerGluHisAsnLysProProLysSer-PheHisGluGluMetLeuGluArgAr 153
 Db 947 CTGAGCAGAACACAGCATTTGCCCGCAGGATCTTATACGAGCATCAACAGCGAGGTG 1006
 QY 153 gAlaGlnGluGlnGlnArgLeuLeuGluAlaLys-----ArgLysG1 168
 Db 1007 AATTATCTCCAGAGCAGCAGACAGTGTATCTAGATCCCTCAGCAGTCCGGAAT 1066
 QY 168 uGluGlnGluArgGluLeuHisGluLeuGlnArgArg-LysGluGluLeuLysG 188
 Db 1067 CCTTGTGAGAGTCTCCCAATCTTGGACAGTCTGAGCAGCAGCCATCTTACGAAAT 1126
 QY 188 luGluLysArgLysGluMetAlaLysGlnGluArgLeuGluLeuAlaSerLeuSerA 208
 Db 1127 CACAAATGTCGAGCCCGAGCTCCAGACACAGAAAGAAATGTCTCAGATCGGAGA 1186
 QY 208 snGlnAspHisThrSerLysLysAspProGlyGly-----HisArgThrAlaAlaI 225
 Db 1187 CCCAGCTCTAT---GATAAAGGTGTCAAAGGTGGAACCTATCCAGCGGCTTACCATGTGT 1243

QY 225 leLeuHisGlyGlySerProAspPheValGlyAsnGlyLysHisArgAlaAsnSerSerG 245
 Db 1244 CTGTGCAT-----CACAAAGACTACAATGATG 1270
 QY 245 lyArgSerArg-----AtgGluArgGlnTyrrSerValCysAsnSerGluAsps 261
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 QY 281 isLysGlyLysCysylleGlySerAspGluGln----- 291
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 QY 292 -----LeuGlyLysLeuValTyrrAsnA 299
 Db 1451 TGCCAACCAATCTCTAGTGTCTCCATCAATTGGCGTCCGGGGAAGCTCTCTG----- 1503
 QY 299 laLeuGluThrAlaThrGlyGlyPheValLeuLeuTyrrGluTrpValLeuGlnTrpGlnL 319
 Db 1504 -----GGTCAAGTGCCTTCGGCAGGGTCTAC-----TTGTCTATGATG 1543
 QY 319 ysLysMetGlyProPheLeuThrSerGlnGluLysGlu-----LysIleAspLysC 336
 Db 1544 TGGACACAGAGCGTGAACCTTCTTAAGCAGGTCCAGTTTGACCCAGATAGTCTCTGAGA 1603
 QY 336 ysLysLysGlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHisP 356
 Db 1604 CAAGCAAGGAGGTGAGTGTCTGGAGTGTGAGATCCAGTTGTCTGAAGAACTTCAGCATG 1663
 QY 356 roAsnValValArgTyrrLeuAlaMetAsnLeuLysGluGlnAspAspSerIleValValA 376
 Db 1664 AGCGCATTTGTGAGTACTACGGTGC-----CTGGGAGCGTGTGAGAAAGATCTCTCAC 1719
 QY 376 spIleLeuValGluHisIleSerGlyValSerLeuAlaHisLeuSerHisSerGlyP 396
 Db 1720 --ATCTTTATGGAGTATATGCCAGGGGCTCTGTAAGACACCATTTGAAGGCTACGGAG 1777
 QY 396 rolleProValHisGlnLeuArgArgTyrrThrAlaGlnLeuLeuSerGlyLysAspTyrrL 416
 Db 1778 CTCTGACAGAGAGTGTGACCCGCAAGTACCCCGGAGATTCTGGAGGCGATGTCTATACC 1837
 QY 416 euHisSerAsnSerValValHisLysValSerAlaSerAsnValLeuValAspAlaG 436
 Db 1838 TGACAGCAACATGATTTGTGCATCGGACATCAAGGAGGCCAATATCTCCGAGACTCAG 1897
 QY 436 luGlyThrVallyslleThrAspTyrrSerIleSerLysArgLeuAlaAspIleCysLysG 456
 Db 1898 CTGGGAATGTGAAGCTTGGGGATTTGGGGCCAGCAACCGCTACAGACCATCTGC----- 1953
 QY 456 luAspValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrr----- 473
 Db 1954 -----ATGTGAGGAGCAGGCATTCG---TCTGTCACTGGCACACCTTACTTGGATGA 2002
 QY 474 -----LysThrGlyLysLysGlyAspValTrpArgLeuGlyL 486
 Db 2003 GTCTTGAAGTATCATGTGGCGAGGCTATGGAAGAAAGGAGCAGCTGTGGAGCTGGGCT 2062
 QY 486 euLeuLeuLeuSer---LeuSerGlnGlyGlnGluCysGlyGluTyrrProval----- 502
 Db 2063 GTACGTGTGTGGAATGTGTACAGAGAAACACCTTGGGAGAGATGTGAAGCTATGGCTG 2122
 QY 503 -----ThrIleProSerAspLeuProAlaA 511
 Db 2123 COATTTTCAAGATTCACCCAGCCTACCAATCTCAGTGTCCCTCTCTCATCTCAGAAC 2182
 QY 511 spPheGlnAspPheLeuLysLysCysValCysLeuAspAspLysGluArgTrpSerProG 531
 Db 2183 ACGGAGGAGCTTCTCTGAGGCG---ATATTTGTGGAAGCTCTGTACAGAGACCTCTAGCTG 2239

531 lnGlnLeuLysHisSerPhe 538
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2240 AGGAGCTGCTCACACACCACTTT 2262

RESULT 14

US-08-461-145C-5
; Sequence 5, Application US/08461145C
; Patent No. 6074861
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, GARY L.
; TITLE OF INVENTION: NOVEL MEKK PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive and Cockfield, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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CURRENT RELEASE NUMBER: US/08/461,145C
 APPLICATION NUMBER: US/08/461,145C
 FILING DATE: 5-JUNE-1995

CLASSIFICATION: 530
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/049,254
 PRIOR APPLICATION DATA: 11 APR 1992

; FILING DATE: 11-APR-1993
 ; PRIOR APPLICATION DATA: 11-APR-1993 450

APPLICATION NUMBER: US 08/323,460
FILING DATE: 14-OCT-1994

; PRIOR APPLICATION DATA: PCT/US94/11690
 ; APPLICATION NUMBER:

FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: PCT/US94/04178

FILING DATE: 15-APR-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/354,516
FILING DATE: 21-FEB-1995

ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.

REGISTRATION NUMBER: P-41,106
REFERENCE/DOCKET NUMBER: CPI-004CN1

TELECOMMUNICATION INFORMATION:
TELEPHONE (617) 227-7400

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

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; INFORMATION FOR SEQ ID NO: 5:
;
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 3089 base pairs
; TYPE: nucleic acid
;

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STRANDEDNESS: single
morphology: linear

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

[illegible]

; LOCATION: 400..2280
US-08-461-145C-5

Alignment Scores:

Length:	2.38e-18
Matches:	284.50

Score:	20.13	Conservative:	39.89%
Percent Similarity:	39.89%	Mismatches:	33.62%

Best Local Similarity: 23.65%
Query Match: 3.33%
Indels: 3.33%

DB: 3
Apps:

US-09-515-806A-2 (1-1649) x US-08-461-145C-5 (1-3089)

QY,
77 valLysCysProProThrTyrProAspValValProGlu

800 CTGGAGTGTGCAGGCGAGTTCCGGATCAAGCGCTTCGCCAGTCTGACGGGGAAATAAATACC
94 AsnAlaLysGlyLeuSerAsnGluSerValAsnLeuLeuLysSerArgLeuGluGluLeu 113
::: ||||| :::
860 TCTACCAAGCTCCTGAGCCGAAGCAGGACCTGTCTGTCA----- 901
::: ||||| :::
114 AlaLysLysHisCysGlyGluValMetIlePheGluLeuAlaTyHisValGlnSerPhe 133
::: ||||| :::
902 GCTCCCAAGAACCCTGGCCGAAGCTCTCTCTCCCCCGG-----GATATGTAC 946
::: ||||| :::
134 LeuSerGluHisAsnLysProProLysSer-PheHisGluGluMetLeuGluArgAr 153
||||| :::
947 CTGAGGGAACAAGCACATTGCCCGCAAGGATCCTATACGAGCATCAACAGCGAAGGTG 1006
||||| :::
153 GalGlnGluGlnArgLeuLeuGluLysLys-----ArgLysGI 168
||||| :::
1007 AATTATCCAGAGACCAGCAACAGTGATGTATGTAGATCCCCTCAGCAGTGCCTGAAAATT 1066
||||| :::
168 uGluGlnGluArgGluLeuHisGluIleGlnArgArg-LysGluGluLysG 188
::: ||||| :::
1067 CTTGTTCAGGAAGCTCCCAATCTTGGACAGGTCAAGCAGACAGGCCCATCTCTTCAGGAAT 1126
::: ||||| :::
188 LuGluLysLysArgLysGluMetAlaLysGlnGluArgLeuGluLeuLeuSerA 208
::: ||||| :::
1127 CACAAATGTCCCGAGCCCGAGGCTTCCACAGAACAAAGAAATGCTCAGATCGGAGA 1186
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208 snGlnAspHisThrSerLysLysAspProGlyGly-----HisArgThrAlaAlaI 225
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225 leLeuHisGlyGlySerProAspPheValIClYAsnGlyLysHisArgAlaAsnSerG 245
::: ||||| :::
1244 CTGTGTCAT-----CACAAAGACTACATGATG 1270
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245 IyArgSerArg-----ArgGluArgGlnTyrrSerValCysAsnSerGluAspS 261
||||| :::
1271 GCAGAAGAACATTTCCCGAATACGACGGCATCAAGGCAACCTATTCTCTGTGGCCCT 1330
::: ||||| :::
261 exProGlySerCysGluLeuLeuTyrrPheAsnMetGlySerProaspGlnLeuMetValH 281
||||| :::
1331 CAAGTCGTCTCTTGAGCACAAATGGCGAGAACATGGGTGTAGCTGTGCAATACCTGGACC 1390
::: ||||| :::
281 iLysGlyLysCysIleGlySerAspGluGln----- 291
::: ||||| :::
1391 CCCGTGGGGCGCTACGGNAGTCACAGATGAGAAATGCCCTACTGTGCAGGAAGGAATG 1450
::: ||||| :::
292 -----LeuGlyLysLeuValTyrrAsnA 299
::: ||||| :::
1451 TGCCAACCAATCTCCTAGTGTCTCCCATCAATTGGCGTCGGGGGAGCTCCTG----- 1503
::: ||||| :::
299 laLeuGluThralaThrGlyGlyPheValLeuLeuTyrrGluTrpValLeuGlnTrpGlnL 319
::: ||||| :::
1504 -----GGTCAAGGTGCCTTCGCGAGGCTAC-----TTGTGCTATGATG 1543
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319 yLysMetGlyProPheLeuThrSerGlnGluLysGlu-----LysileAspLysC 336
::: ||||| :::
1544 TGCACACAGGACGTGAACCTTGCTTAAGAGGGTCCAGTTTGACCCAGATAGCTCTGAGA 1603
::: ||||| :::
336 ysLysLysGlnIleGlnGlyThrGluThrGluPheAsnSerLeuValLysLeuSerHisP 356
::: ||||| :::
1604 CAAGCAAGGAGGTGAGTGTCTTGGAGTGTGAGATCCAGTTCCTGAAGAACCTCGACGATG 1663
::: ||||| :::
356 roAsnValValArgTyrrLeuAlaMetAsnLeuLysGluInAspAspSerIleValValA 376
::: ||||| :::
1664 AGGCATTTGTGAGTAGTACTACGGCTGC--CTCGGGACCGTGTGAGAGAGATCTCACC- 1719
::: ||||| :::
376 spIleLeuValGluHisIleSerGlyValiserLeuAlaHisLeuSerHisSerGlyP 396
::: ||||| :::
1720 --ATCTTTATGGAGTATATGCCAGGGGGCTCTGTAAAAAGACCAGTGTGAAGGCCCTACGGAG 1777
::: ||||| :::
396 rolleproValHisGlnLeuArgArgTyrrThrAlaGlnLeuLeuSerGlyLeuAspTyrl 416
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US-09-515-806A-2 (1-1649) x US-08-628-829-9 (1-3089)

Qy	77	ValLysCysProThrTyTyrProAspValValProGluIleGlu	LeuLys 93
Db	800	CTGGAGTGTCCAGGAGGTTCCGATCAAGCCTTCCAGTCTGCAGGGGATATAAATACCA	859
Qy	94	AsnAlaLysGlyLeuSerAsnGluSerValAsnLeuLeuLysSerArgLeuGluGluLeu	113
Db	860	TCTACCAAGCTCTGAGCCAGAGACGAGCACCTGCTCTGCA	901
Qy	114	AlaLysLysHisCysGlyGluValMetIlePheGluLeuAlaTyrHisValGlnSerPhe	133
Db	902	GCTCCCAACCCCTGGCGGAGTCTCTCTCCCGCGG	946
Qy	134	LeuSerGluHisAsnLysProProLysSerPheHisGluGluMetLeuGluLysArg	153
Db	947	CTGAGCGACACACACATTCGCCGCAAGGATCTTATACGAGCATCAACACGGAAGGTG	1006
Qy	153	GalaGlnGluGlnGlnArgLeuLeuLys	168
Db	1007	AATTCATCCAGACAGCGAAGTGTATGCTAGATCCCTCAGCAGTGCCGAAAT	1066
Qy	168	uGluGlnGluArgGluIleLeuHisGluIleGlnArgArgLysGluGluLeuLysG	188
Db	1067	CTTGTCAGGAAGCTGCAATCTTGACAGCTCAGCAGACGCCCATCTCTTCAGGAAT	1126
Qy	188	luGluLysLysArgLysGluMetAlaLysGlnGluArgLeuGluIleAlaSerLeuSerA	208
Db	1127	CACAAATGTCGAGCCGAGCTTCCAGACAAACAGAAAGAAATGTCAGATCGGAGA	1186
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Qy	261	erProGlySerCysGluIleLeuTyrPheAsnMetGlySerProAspGlnLeuMetValH	281
Db	1331	CAAGTCGCTCTTGAGCACAAATGGCGAGAACATGGGTGTAGTGTGCAATACCTGGACC	1390
Qy	281	isLysGlyLysCysIleGlySerAspGluGln	291
Db	1391	CCCCTGGCGCCTACGGAGTGCAGACGTGAGATGCCCTCACTGTGCAGGAAGAAATG	1450
Qy	292		1450
Db	1451	TGCCAACCAATCTCTAGTGTCCCATCAATTGGCGTCGGGGAGCTCCTG	1503
Qy	299	laLeuGluThrAlaThrGlyGlyPheValLeuLeuTyrCluTrpValLeuGlnTrpGlnL	319
Db	1504	-----GGTCAAGTGCCTTCGGCAGGCTCTAC-----TTGTGCTATGATG	1543
Qy	319	ysLysMetGlyProPheLeuThrSerGlnGluLysGlu	336
Db	1544	TGCACACAGCGTGAACCTTGTCTTCAAGCAGGTCCAGTTTGACCCAGATAGTCTCTGAGA	1603
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Db	1604	CAAGCAAGGAGGTGAGTGCTCTGGAGTGTGAGATCCAGTTGCTGAAGAACCTGCAGCATG	1663
Qy	356	roAsnValValargTyrLeuAlaMetAsnLeuLysGluGlnAspAspSerIleValValA	376
Db	1664	AGCGCATTTGCAGTACTACGGCTGC---CTGCGGACCGTGTGAGAAATCTCTCACC-	1719
Qy	376	spileuValGluHisIleSerGlyValSerLeuAlaAlaHisLeuSerHisSerGlyP	396
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us-09-515-806a-2.rni

Thu Jun 12 14:34:04 2003

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396 roileproValHisGlnLeuArgTyrThrAlaGlnLeuLeuSerGlyLeuAspTyrL 416
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QY      :|||:|||||:|||||:|||||:|||||:|||||:|||||:
436 luGlyThrValLysIleThrAspTyrSerIleSerLysArgLeuAlaAspIleCysLysG 456
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY      :|||:|||||:|||||:|||||:|||||:|||||:|||||:
456 luAspValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyr----- 473
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1954 -----ATGTCAGGACAGGCAATTGCG-----TCTGTCACTGGGCACACCTACTGGATGA 2002
QY      :|||:|||||:|||||:|||||:|||||:|||||:|||||:
474 -----LysThrGlyLysLysGlyAspValTrpArgLeuGlyL 486
Db      :|||:|||||:|||||:|||||:|||||:|||||:|||||:
2003 GTCTGTAAGTCATCAGTGGGGGGCTATGGAGAGGAGGAGCGTGTGGAGCCTGGGCT 2062
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486 euLeuLeuLeuSer---LeuSerGlnGlyGlnGluCysGlyGluTyrProVal----- 502
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2123 CCATTTTCAAGATTGCCACCGCGCTACCAATCTCAGCTGGCCTCTCACATCTCAGAAC 2182
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2183 ACGGCAGGAGCTTCTCTGAGGCGC---ATATTGTGGAAGCTGTCAGAGACCCCTCAGCTG 2239
QY      :|||:|||||:|||||:|||||:|||||:|||||:|||||:
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2240 AGGAGCTGCTCACACCACTTT 2262

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Search completed: June 12, 2003, 08:33:25
Job time : 13129 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 12, 2003, 04:43:30 ; Search time 937 Seconds
(without alignments)
2463.007 Million cell updates/sec

Title: US-09-515-806A-2

Perfect score: 8544

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Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -THR MAX=100
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Published Applications NA:
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15: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	8319.5	97.4	4989	9	US-09-842-758-3
3	4295	50.3	2946	9	US-09-836-392-6
4	3029	35.5	2200	10	US-09-925-301-184

Alignment Scores:

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ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/09515806
; Patent No. US20020132321A1

; GENERAL INFORMATION:
; APPLICANT: COOK, WILLIAM J.

; TITLE OF INVENTION: 14790. NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR

; FILE REFERENCE: 38155-20002.00

; CURRENT APPLICATION NUMBER: US/09/515,806

; CURRENT FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 5525

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (63)..(4991)

US-09-515-806-1

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Sequence 753, App
Sequence 24436, A
Sequence 1, Appli
Sequence 101, App
Sequence 12737, A
Sequence 105, App
Sequence 103, Appl
Sequence 107, Appl
Sequence 3, Appli
Sequence 1707, Ap
Sequence 23, Appl
Sequence 147, App
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Sequence 1180, Ap
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QY	1101	AlaAlaLeuPheMetAspHisSerClyMetLeuValMetLeuProPheAspLeuArgIle	1120
DB	3363	GCTGCCCTATTCCATGGACCAACAGCGGGATGCTGGTGATGCTCTCTTTGACCTGCGGATC	3422
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DB	3423	CCTTTGTCCAGAGATATGTGCGAAGAAATAATATTTGAATTTTAAACGACATCTGCATAGAA	3482
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DB	3483	CGTGTGTTTCAGGCCCGCAACTAGATCGATTTTCATCCCAAAGAACTTCTGAGGTGTGCA	3542
QY	1161	PheAspIleValThrSerThrAsnSerPheLeuProThrAlaGluIleIleTyrThr	1180
DB	3543	TTTGATATTGACATCTTACCACCAACAGCTTTCTGCCACTGCTGAAATATATCTACACT	3602
QY	1181	IleTyrGluIleIleGlnGluPheProAlaLeuGlnGluArgAsnTyrSerIleTyrIleu	1200
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DB	3663	AACCATACCATGTTATTGAAGCAATACTCTTTACACTGTGGCATCCAGAAGATAAATC	3722
QY	1221	SerGlnValTyrIleLeuTyrAspAlaValThrGluLysLeuThrArgArgGluVal	1240
DB	3723	AGTCAAGTCTACATATTCTGTATGATGCTGTGACAGAGAAGCTGCAGAGAGAAGTG	3782
QY	1241	GluAlaLysPheCysAsnLeuSerLeuSerSerAsnSerLeuCysArgLeuTyrLysPhe	1260
DB	3783	GAAGCTAAATTTTGTAAATCTGCTTTTGCTCTTAATAGTCTGTGCTGACTTACAAGTTT	3842
QY	1261	IleGluGlnLysClyAspLeuGlnAspLeuMetProThrIleAsnSerLeuIleLysGln	1280
DB	3843	ATTGACAGAGGGAGATTGCAAGATCTTATGCCAACATAAATTCATTAATAAACAG	3902
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us-09-515-806a-2.rnpb

Thu Jun 12 14:34:05 2003

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 1581 LysGluThrIleLeuGlnPheLeuSerLeuGluThrAspAlaAspGluGlnAlaPheAsn 1600
 4803 AAGAAGAAACAATATTACAGTTTTTATCATATGAGTGGGATGCTGATGACAGGCAATTAAC 4862
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US-09-515-806A-2 (1-1649) x US-09-842-758-3 (1-4989)
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 QY 41 LeuArgProAspAlaCysGlyPro-----ValLysGluProProGluIleAsnLeuVal 58
 Db 121 CTGCGCGCGGCGCTTGGCGACCGGTAAAGTTCAGAGAGCCCTCTGAAATCAATTTAGTT 180
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 Db 241 TGCCACCTACCTATCCAGATGTAGTTCTGAAATAGAGTTAAAAATGCCAAAGGTCTTA 300
 QY 99 SerAsnGluSerValAsnLeuLeuLysSerArgLeuGluGluLeuAlaLysHisCys 118
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 NUMBER OF SEQ ID NOS: 113
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: 60/265,160
 PRIOR FILING DATE: 2001-01-22
 PRIOR APPLICATION NUMBER: 60/263,217
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: 60/232,678
 PRIOR FILING DATE: 2000-07-25
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 PRIOR APPLICATION NUMBER: 60/201,236
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 60/201,006
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 60/200,780
 PRIOR FILING DATE: 2000-04-26
 PRIOR APPLICATION NUMBER: 60/200,613
 PRIOR FILING DATE: 2000-04-25
 CURRENT FILING DATE: 2001-04-25
 PRIOR APPLICATION NUMBER: 60/200,158

RESULT 2
 US-09-842-758-3
 Sequence 3, Application US/09842758
 Publication No. US20030083244A1
 GENERAL INFORMATION:
 APPLICANT: Vernet, Corine A. M.
 APPLICANT: Fernandes, Elma R.
 APPLICANT: Gerlach, Valerie
 APPLICANT: Shimkets, Richard A.
 APPLICANT: Malyankar, Uriel M.
 APPLICANT: Boldog, Ferenc L.
 APPLICANT: Zerhusen, Bryan D.
 APPLICANT: Spytek, Kimberly A.
 APPLICANT: Majumder, Kumud
 APPLICANT: Tchernev, Velizar T.
 APPLICANT: Padigaru, Muradidhara
 APPLICANT: Patturajan, Meera
 APPLICANT: Burgess, Catherine E.
 APPLICANT: Gangolli, Esha A.
 APPLICANT: Smithson, Glenna
 APPLICANT: Rastelli, Luca
 APPLICANT: MacDougall, John R.
 APPLICANT: Taupier, Raymond J.
 APPLICANT: Grosse, William M.
 APPLICANT: Edward, Szekeres S.
 APPLICANT: Alsobrook II, John P.
 TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
 FILE REFERENCE: 15966-783
 CURRENT APPLICATION NUMBER: US/09/842,758

QY	495	nGluCysGlyGluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPh	515
Db	1500	GGAAATGTGGAGATACCTCTGACCAATCCTAGTGACTTTACCAGCTGACTTTCAAGATT	1559
QY	515	eLeuLysLys---CysValCysLeuAspAspLysGluArgTrpSerProGlnGlnLeuLe	534
Db	1560	TCTAAGGAGAGATGTGTGTGCTTGATGACAAGGAAAGATGGAGTCCCGACAGATTGTT	1619
QY	534	uLysHisSerPheIleAsnProGlnProLysMetProLeuValGluGlnSerProGluAs	554
Db	1620	GAACACAGCTTTATAATCCCGACCAAAATGCCTCTAGTGAAACAAAGTCCTGAA--	1677
QY	554	pSerGlyGlyGlnAspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAl	574
Db	1678	-TCTGAAGGACAAGATTATGTTGAGACTGTTATTTCTAGCAACGGGTACCCAGTGTGC	1736
QY	574	aPhePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGluPheGluGluLeuGl	594
Db	1737	CTTCTTTAGTGAGACACAGACAGACTTTTCCGATACTTCATTGAGTTTGAAGAATTACA	1796
QY	594	nLeuLeuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCy	614
Db	1797	ACTCTTGTTGAAGGAGCTTTTGAGCTGTCTATCAAGGTGCAGAACAAAGTTGCAACG	1856
QY	614	sCysTyrAlaValLysArgIleProIleAsnProAlaSerArgGlnPheArgArgIleLy	634
Db	1857	CTGCTACCGCAGTGAAGCGCATCCCAATCAACCGCGCAGCGGAGTTCGAGAGATCAA	1916
QY	634	sGlyGluValThrLeuLeuSerArgLeuHisGluAsnIleValArgTyrTyrAsnAl	654
Db	1917	GGCGCAAGTGACACTGTGTGTACGGCTGCACCATGAGAACATTGTGCGCTACTACAACG	1976
QY	654	aTrpIleGluArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyPr	674
Db	1977	CTGGATCGAGCGGCAGCGCGCGGGACCGGGACCGCGCGCGGACTCCGGGCC	2036
QY	674	oLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeuAs	694
Db	2037	CTGGCCAAAGATGACCGAGCTGCACGGGGCAGCGCGGAGCGACACAGCGCTGGA	2096
QY	694	pSerValGluAlaAlaProProIleLeuSerSerSerValGluTrpSerThrSe	714
Db	2097	CAGCGTAGCGCGCGCGCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC	2156
QY	714	rGlyGluArgSerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspAspGl	734
Db	2157	GGCGAGCGCTCGGCAGTGCCGTTTCCCGCCACCGCGCCCGGCTCCAGCGATGACGA	2216
QY	734	uAspAspGluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAs	754
Db	2217	GGACGACGACGAGACGAGCAGCGTGGCGTCTCTCCAGTCTCTTCGTGCTGTCTAGA	2276
QY	754	pSerGluSerAspIlePheAspAsnGluAspGluAsnSerLysSerGlnAsnGlnAs	774
Db	2277	TTCTGAAGTGTATATCTTTGCAATGAAGATGAGAACAGTAAAGATCAGATCAGGA	2336
QY	774	pGluAspCysAsnGluLysAsnGlyCysHisGluSerGluProSerValThrThrGluAl	794
Db	2337	TGAAGATTGCAATGAAAGAATGGCTGCCATGAAAGTGAGCCATCAGTGACACTGAGG	2396
QY	794	aValHisTyrLeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIle	814
Db	2397	TGTGCACCTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGACACCA	2456
QY	814	eAspGlnGlyLeuTyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAs	834
Db	2457	TGACCGAGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTCGAGAGATTCGGA	2516
QY	834	pGlyLeuAlaTyrIleHisGluLysGlyWetIleHisArgAspLeuLysProValAsnIle	854
Db	2517	TGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGATTTGAAGCCTGTCAACAT	2576

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QY	854	ePheLeuAspSerAspAspHisVallylleGlyAspPheGlyLeuAlaThrAspHisLe	874
Db	2577	TTTTTTGGATTCTGATGACCATGTGAAATAGGTGATTTTGGTTGGCGACAGCATCT	2636
QY	874	uAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSerAspPr	894
Db	2637	AGCTTTTCTGCTGACACCAACCAAGACGATCAGACAGGAGACTTGAATTAAGTCAGACCC	2696
QY	894	oSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnG	914
Db	2697	TTTCAGGTCACTTAACCTGGGATGGTTGGCACTGCTCTCTATGTAAGCCAGGATCCCAAG	2756
QY	914	ySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyllePhePh	934
Db	2757	AAGCACCAAAATCTGCATACACACAGAAAGTGGATCTCTTCAGCTGGGAATATCTTCTT	2816
QY	934	eGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLe	954
Db	2817	TGAGATGCTCATCACCCATGGTCAGGCTTCAGAAAGGATCTTTGTTCTCAACCAACT	2876
QY	954	uArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHisAlaLysG	974
Db	2877	CAGAGATCCCACTTCGCTGAAGTTTCCAGAGACTTTGACGATGGAGAGCATGCAAGCA	2936
QY	974	nLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrG	994
Db	2937	GAATCAGTCATCTCTGGCTGTGTAACCAACGATCCAGCAAAACGGCCACAGCCACAGA	2996
QY	994	uLeuLeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHisGluVa	1014
Db	2997	ACTGCTCAAGAGTGAGCTGCTGCCCCACCCAGATGGAGAGTCAGAGCTGCATGAAGT	3056
QY	1014	lLeuHisHisThrLeuThrAsnValAspGlyLysAlaTyrArgThrMetMetAlaGlnI	1034
Db	3057	GCTGCACCAACAGCTGACCAACGCTGGATGGGAAGCCCTACCGCACCATGATGGCCAGAT	3116
QY	1034	ePheSerGlnArgIleSerProAlaIleAspTyrThrTyrAspSerAspIleLeuLysG	1054
Db	3117	CTTCTCGCAGCGCATCTCCCTGCCATTCGATTAACCTATGACAGGCACATCTGAAGG	3176
QY	1054	yAsnPheSerIleArgThrAlaLysMetGlnGlnHisValCysGluThrIleIleArgI	1074
Db	3177	CAACTTCTCAATCCGTACAGCAAGATGCAGCAGCATGTGTGAACCATCATCCGCAT	3236
QY	1074	ePheLysArgHisGlyAlaValGlnLeuCysThrProLeuLeuProArgAsnArgG	1094
Db	3237	CTTTAAAGACATGGTGTCTTCAGTTGTGTACTCCACTACTGCTTCCCCGAAACACACA	3296
QY	1094	nIleTyrGluHisAsnGluAlaLeuPheMetAspHisSerGlyMetLeuValMetLe	1114
Db	3297	AAATATATGACACCAACGAAGCTGCCCTATTTCATGGACACACAGCGGATGCTGGTGTCT	3356
QY	1114	uProPheAspLeuArgIleProPheAlaArgTyrValAlaArgAsnAsnIleLeuAsnLe	1134
Db	3357	TCCTTTTCACCTCGCGGTGCTTTTGAAGATATGTCGAAGAAATATATATATGAATTT	3416
QY	1134	uLysArgTyrCysIleGluArgValPheArgProArgLysLeuAspArgPheHisProly	1154
Db	3417	AAAACGGTACTGCAAGAACGTGTTCACCGCCGCGCAAGTTAGATCGATTTTCATCCCA	3476
QY	1154	sGluLeuLeuGluCysAlaPheAspIleValThrSerThrThrAsnSerPheLeuProth	1174
Db	3477	AGAACTTCCTGGAGTGTGCTTTGATATTTGTCATCTTACCAACCAACAGCTTTCGCCAC	3536
QY	1174	rAlaGluIleIleTyrThrIleTyrGluIleGlnGluPheProAlaLeuGlnGluArg	1194
Db	3537	TGCTGAATATATCTACACTATCTATGAATCATCCAGAGTTTCCAGCATCTTCAAGAAAG	3596
QY	1194	gAsnTyrSerIleTyrLeuAsnHisThrMetLeuLysAlaIleLeuLeuHisCysG	1214
Db	3597	AAATTACAGTATTTATTTGAACCATACCAATGATTTTGAAGCAATATCTTACACTGTGG	3656
QY	1214	yIleProGluAspLysLeuSerGlnValTyrIleIleLeuTyrAspAlaValThrGluLy	1234

Db	3657	GATCCAGAGATATAACTCAGTCAAGTCTACATATTCTGTATGATGCTGTGACAGAGAA	3716
QY	1234	sLeuThrArgArgGluValGluAlaLysPheCysAsnLeuSerLeuSerSerAsnSerLe	1254
Db	3717	GCTGACGAGGAGAGAGTGGAAAGCTAAATTTTGTAAATCTGTCTTTCTCTTAATAGTCT	3776
QY	1254	uCysArgLeuTyrLysPheIleGluGlnLysGlyAspLeuGlnAspLeuMetProThrI	1274
Db	3777	GTGTGCACTCTACAAAGTTTATTGAAACGAGAGGAGATTTGCAAGATCTTATGCAACAAT	3836
QY	1274	eAsnSerLeuIleLysGlnLysThrGlyIleAlaGlnLeuValLysTyrGlyLeuLysAs	1294
Db	3837	AAATTCATTAATAGAACAGAAACAGAGTATTCGACAGTTGTTGAAGTATGGCTTAAAGA	3896
QY	1294	pLeuGluGluValValGlyLeuLeuLysLysLeuGlyIleLysLeuGln-----Valle	1312
Db	3897	CCTAGAGGAGGTTGTTGGACTGTGTAAGAACTCGGCATCAAGTTACAGGTTTGGGTCCT	3956
QY	1312	uIleAsnLeuGlyLeuValTyrLysValGlnGlnHisAsnGlyIleIlePheGlnPheVa	1332
Db	3957	GATCAATTTGGGCTTGGTTTACAAAGGTGCAGCAGCACAATGAATCATCTTCCAGTTTGT	4016
QY	1332	lAlaPheIleLysArgArgGlnArgAlaValProGluIleLeuAlaAlaGlyGlyArgTy	1352
Db	4017	GGCTATCATCAACGAAAGGCAAGGCTGTACCTGAATCTCTCGCAGCTGGAGGAGATA	4076
QY	1352	rAspLeuLeuIleProGlnPheArgGlyProGlnAlaLeuGlyProValProThrAlaI	1372
Db	4077	TGACCTGCTGATTTCCCGCTTTAGAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCAT	4136
QY	1372	eGlyValSerIleAlaIleAspLysIleSerAlaAlaValLeuAsnMetGluGlu-----	1390
Db	4137	TGGGCTCAGCATAGCTATAGACAGATATCTGTCTGTCTCTCAACATGGAGAAATCTCT	4196
QY	1391	----SerValThrIleSerSerCysAspLeuLeuValValSerValGlyGlnMetSerMe	1409
Db	4197	AGTCTGTGTACAAATAGGCTCTGGGGACCTCTGGTTGTAAAGTGTGGCCAGATGTCTAT	4256
QY	1409	tSerArgAlaIleAsnLeuThrGlnLysLeuThrThrAlaGlyIleThrAlaGluIleMe	1429
Db	4257	GTCACGGGGCCATAAACCTAACCCAGAAATCTGTGACAGCAGGCATCATCAGCAAAATCAT	4316
QY	1429	tTyrAspTrpSer-----GlnSerGlnGluGluGlnGluTyrCysArgHisG	1447
Db	4317	GTACGACTGTCTACAGTCTTCAGTCCCAAGAGAAATTTACAGAGTACTGCAGACATCATGA	4376
QY	1447	uIleThrTyrValAlaLeuValSerAspLysGluGlySerHisValLysValLysSerPh	1467
Db	4377	AATCACCTATGTGGCCCTTGTCTCGGATAAAGAGGAGCCATGTCAAGGTTAAAGTCTTT	4436
QY	1467	eGluLysGluArgGlnThrGluLysArgValLeuGluThrGluLeuValAspHisValLe	1487
Db	4437	CGAAGAGGAAAGGACAGACAGAGAGCGTGTCTGGAGACTGAACTTGTGGACCATGTACT	4496
QY	1487	uGlnLysLeuArgThrLysValThrAspGluArgAsnGlyArgGluAlaSerAspAsnLe	1507
Db	4497	GCAGAAACTGAGGACTAAAGCTCATGATGAAAGAAATTTTAGAGAGAGCTTCCGTAATCT	4556
QY	1507	uAlaValGlnAsnLeuLysGlySerPheSerAsnAlaSerGlyLeuPheGluIleHisG	1527
Db	4557	TGCAGTGCAAAATCTGAAAGGGGTCAATTTCTAATGCTTCAGGTTTGTGTTGAAATCCATCG	4616
QY	1527	yAlaThrValValProIleValSerValLeuAlaProGluLysLeuSerAlaSerThrAr	1547
Db	4617	AGCAACAGTGTGTTCCCATTTGTGAGTGTGTAGCCCGGAGAGGCTGTACCCAGCAGCTAG	4676
QY	1547	gArgArgTyrGluThrGlnValGlnThrArgLeuGlnThrSerLeuAlaAsnLeuHisG	1567
Db	4677	GAGCGCTATGAACCTCAGGTACAACTCGACTTCAGACCTCCCTGCCAATCTTACATCA	4736
QY	1567	nLysSerSerGluIleGluIleLeuAla---ValAspLeuProLysGluThrIleLeuG	1586

Db 4737 GAAAGACAGTGAAATTGAAATTCCTGGCTGTAGTGTACCTACCCAAAGAAACAAATATTACA 4796
 QY 1586 nHeLeuSerLeuGluTrpAspAlaAspGluGlnAlaPheAsnThrThrValIysGlnLe 1606
 Db 4797 GTTITATCATAGAGTGGATGCTGATGAAACAGGCAATTAAACAACTGTGAACGAGCT 4856
 QY 1606 uLeuSerArgLeuProLysGlnArgTyrLeuLysLeuValCysAspGluIleTyrAsnI 1626
 Db 4857 GCTGTCACGCTGCCAAGCAAGATACCTCAATTAATAGTCTGTGATGAATTTATAACAT 4916
 QY 1626 eLysValGluLysLysValSerValLeuPheLeuTyrSerTyrArgAspAspTyrTyr 1646
 Db 4917 CAAAGTAGAARAAAGTGTCTGTCTATTTCTGTACAGTATAGAGATGACTACTACAG 4976
 QY 1646 gileLeuPhe 1649
 Db 4977 AATCTTATTT 4986

RESULT 3

US-09-836-392-6
 ; Sequence 6, Application US/09836392
 ; Patent No. US20020173458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides, a
 ; FILE REFERENCE: PT020P1
 ; CURRENT APPLICATION NUMBER: US/09/836,392
 ; PRIOR FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/28066
 ; PRIOR FILING DATE: 2000-10-11
 ; PRIOR APPLICATION NUMBER: 60/159,542
 ; PRIOR FILING DATE: 1999-10-15
 ; PRIOR APPLICATION NUMBER: 60/165,914
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 60/189,027
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 2946
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-836-392-6

Alignment Scores:
 Pred. No.: 0 Length: 2946
 Score: 4295.00 Matches: 841
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.27% Indels: 0
 DB: 9 Gaps: 0

US-09-515-806A-2 (1-1649) x US-09-836-392-6 (1-2946)

QY 809 ThrLeuArgAspThrIleAspGlnGlyLeuTyrArgAspThrValArgLeuTrpArgLeu 828
 Db 14 ACTTTACGACACACCATTCAGGAGCTGTATCGAGACACCGTCAGACTCTGAGGCTT 73
 QY 829 PheArgGluLeuLeuAspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAsp 848
 Db 74 TTTTCGAGAGATTCTGGATGATTAGCTTATATCATCATGAGAAAGAAATGATTCACCGGGAT 133
 QY 849 LeuLysProValAsnIlePheLeuAspSerAspAspHisValLysIleGlyAspPheGly 868
 Db 134 TTGAGCCCTGTCAACATTTTGGATTCTGTGATGACCATGTGAATAGTGTATTTTGT 193
 QY 869 LeuAlaThrAspHisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAsp 888
 Db 194 TTGGGACAGACCACTAGCTTTTCTGCTGACAGCAACAAACACATCAGACAGGAGAC 253
 QY 889 LeuIleLysSerAspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrVal 908

Db 254 TTGATTAAAGTACAGCCCTTACAGTCACTTAACCTGGGATGCTTGGCACTGCTCTCTATGTA 313
 QY 909 SerProGluValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSer 928
 Db 314 AGCCCAAGAGTCCCAAGGAGCACCACCAATCTGCATACACAGAAAGTGGATCTCTTCAGC 373
 QY 929 LeuGlyIleIlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIle 948
 Db 374 CTGGGAATTTATCTTTCTTTGAGATGCTCTATCACCCTCATGCTCAGGCTTCAGAAAGGATC 433
 QY 949 PheValLeuAsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAsp 968
 Db 434 TTTGTTCTCAACCAACTCAGATCCCACCTTCGCTTAAGTTTCCAGAAGACTTTGACAT 493
 QY 969 GlyGluHisAlaLysGlnLysSerValIleSerTyrLeuLeuAsnHisAspProAlaLys 988
 Db 494 GGAGAGCATGCAAGAGCAGAAATCAGTCATCTCTGCTGTTGAACCAAGATCCAGCAAAA 553
 QY 989 ArgProThrAlaThrGluLeuLysSerGluLeuLeuProProProGlnMetGluGlu 1008
 Db 554 CGGCCACACGACACAGACTGCTCAAGAGTGAGCTGCTGCCCTCCACCCACCCAGATGGAG 613
 QY 1009 SerGluLeuHisGluValLeuHisThrLeuThrAsnValAspGlyLysAlaTyrArg 1028
 Db 614 TCAGAGTGCATGAAGTGTGTCACACACGCTGACCAACGTTGGATGGAGAGCCCTACCCG 673
 QY 1029 ThrMetMetAlaGlnIlePheSerGlnArgIleSerProAlaIleAspTyrThrTyrAsp 1048
 Db 674 ACCATGATGCCACAGATCTTCTCGCAGGCGATCTCCCTGCTGCTGATTCGATTCACCTATG 733
 QY 1049 SerAspIleLeuLysGlyAsnPheSerIleArgThrAlaLysMetGlnGlnHisValCys 1068
 Db 734 AGCGACATAGTGAAGGCAACTTCTCAATCGGTACACCAAGATGCGAGCAGATGTGTGT 793
 QY 1069 GluThrIleIleArgIlePheLysArgHisGlyAlaValGlnLeuCysThrProLeuLeu 1088
 Db 794 GAAACCATCATCCGATCTTTAAAGACATGGAGCTGTTTCAGTTGTGTACTCTCCACTACTG 853
 QY 1089 LeuProArgAsnArgGlnIleTyrGluHisAsnGluAlaAlaLeuPheMetAspHisSer 1108
 Db 854 CTTCCCGAAACAGACAAATATATAGCACACAGAGCTGCCCTATTTCATGACACACAGC 913
 QY 1109 GlyMetLeuValMetLeuProPheAspLeuArgIleProPheAlaArgTyrValAlaArg 1128
 Db 914 GGGATGCTGTGATGCTTCTTTTGGACCTCGGATCCCTTTTGCAGATATGTCGCAAGA 973
 QY 1129 AsnAsnIleLeuAsnLeuLysArgTyrCysIleGluArgValPheArgProArgLysLeu 1148
 Db 974 AATAATATATTGAATTTAAACCGATATCTGCATAGACGTTGTTTCAGGCCCGCGCAAGTTA 1033
 QY 1149 AspArgPheHisProLysGluLeuLeuGluCysAlaPheAspIleValThrSerThrThr 1168
 Db 1034 GATCGATTTCTCCAAAGAACTTCTGGAGTGTGATTTGATTTGTCACCTTCTACACC 1093
 QY 1169 AsnSerPheLeuProThrAlaGluIleIleTyrThrIleTyrGluIleIleGlnGluPhe 1188
 Db 1094 AACAGCTTTCTGCCACTCTCTGAATTTATCTACACTATCTATGAATCATCTCAAGATCTT 1153
 QY 1189 ProAlaLeuGlnGluArgAsnTyrSerIleTyrLeuAsnHisThrMetLeuLeuLysAla 1208
 Db 1154 CCAGCACTTCAGAAAGAAATTTACAGTATTTATTGAAACCATCATGTTTATTGAAGCA 1213
 QY 1209 IleLeuLeuHisCysGlyIleProGluAspLysLeuSerGlnValTyrIleIleLeuTyr 1228
 Db 1214 ATACTCTACACTGTGGGATCCAGAGATTAACCTCAGTCAAGTCTACATTTATCTGTAT 1273
 QY 1229 AspAlaValThrGluLysLeuThrArgGluValGluAlaLysPheCysAsnLeuSer 1248
 Db 1274 GATGCTGTGACAGAGAAAGCTGACGAGGAGAGAAAGTGAAGCTAAATTTTGTAACTGTCT 1333
 QY 1249 LeuSerSerAsnSerLeuCysArgLeuTyrLysPheIleGluGlnLysGlyAspLeuGln 1268
 Db 1334 TTGCTCTCTATAGTGTGTGCTGACTCTCAAGTTTATTGAACAGAGGAGAGATTGCAA 1393

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1629 GluLysValSerValLeuPheLeuTyrSerTyrArgAspTyrTyrArgIleLeu 1648
 2474 GAAAAAAGGTGTCTGTGCTATTTCGTACAGCTATAGAGATGACTTACTACAGAATCTTA 2533

QY 1269 AspLeuMetProThrIleAsnSerLeuIleLysGlnLysThrGlyIleAlaGlnLeuVal 1288
 Db 1394 GATCTTATGCCAACAAATAATTCATTATAAACAAGAAACAGGTATGACAGTGGTG 1453
 QY 1289 LysTyrGlyLeuAspLeuGluValValGlyLeuLeuLysLysLeuGlyIleLys 1308
 Db 1454 AAGTATGGCTTAAAGACCTAGAGGAGGTGTGACTGTGTGAAGAACTCGGCATCAAG 1513
 QY 1309 LeuGlnValLeuIleAsnLeuGlyLeuValTyrLysValGlnGlnHisAsnGlyIle 1328
 Db 1514 TTACAGGTCTTGATCAATTTGGCTTGGTTTACAAAGGTGCAGCAGCAATGGAATCATC 1573
 QY 1329 PheGlnPheValAlaPheLeuLysArgArgGlnArgAlaValProGluLeuLeuAla 1348
 Db 1574 TTCAGTTTGTGGCTTTCATCAACACGAGGCAAGGCTGTACCTGGAATCTCGAGCT 1633
 QY 1349 GlyArgTyrAspLeuLeuIleProGlnPheArgGlyProGlnAlaLeuGlyProVal 1368
 Db 1634 GGAGGCAGATATGACCTGCTGTATCCAGTTTACAGGCGCCCAAGCTCTGGGGCCAGTT 1693
 QY 1369 ProThrAlaIleGlyValSerIleAlaIleAspLysIleSerAlaAlaValLeuAsnMet 1388
 Db 1694 CCGACTGCCATTGGGTGAGTATGATAGCAAGATATCTGCTGCTCTCAACATG 1753
 QY 1389 GluGlnSerValThrIleSerSerCysAspLeuValValSerValGlyGlnMetSer 1408
 Db 1754 GAGGAATCTGTTCATTAAGCTCTGTGACCTCTGTTGTTAAGTGTGGCCAGATGTCT 1813
 QY 1409 MetSerArgAlaIleAsnLeuThrGlnLysLeuThrAlaGlyIleThrAlaGluIle 1428
 Db 1814 ATGTCAGGGCCATCAACCTTAACCCAGAACTCTGGACAGCGCATCACAGCAAAATC 1873
 QY 1429 MetTyrAspTrpSerGlnSerGlnGluLeuGlnGluTyrCysArgHisHisGluIle 1448
 Db 1874 ATGTACGACTGTGTACATCCAGAGAGAAATTCAGAGTACTGCAGACATCATGAATC 1933
 QY 1449 ThrTyrValAlaLeuValSerAspLysGluGlySerHisValLysValLysSerPheGlu 1468
 Db 1934 ACCTATGTGGCTTGTCTCGGATAAAGAGGAGCCATGTCAAGGTTAAGTCTTTCGAG 1993
 QY 1469 LysGluArgGlnThrGluLysArgValLeuGluThrGluLeuValAspHisValLeuGln 1488
 Db 1994 AAGGAAAGCAGACAGAGAGGCTGTGTGGAGACTGAACTTGTGGACCATGTACTGCAG 2053
 QY 1489 LysLeuArgThrLysValThrAspGluArgAsnGlyArgGluAlaSerAspAsnLeuAla 1508
 Db 2054 AAATGAGGACTAAAGTCACTGATGAAGGAATGGCAGAGAGCTTCGATAATCTTGCA 2113
 QY 1509 ValGlnAsnLeuLysGlySerPheSerAsnAlaSerGlyLeuPheGluIleHisGlyAla 1528
 Db 2114 GTGCAAAATCTGAAGGGGTCAATTTCTTAATGCTTCAGTTTGTGTTGAAATCCATGGAGCA 2173
 QY 1529 ThrValValProIleValSerValLeuAlaProGluLysLeuSerAlaSerThrArg 1548
 Db 2174 ACAGTGTTCCTTGTGAGTGTGTGCTAGCCCGAGAGAGCTGTCCAGCCAGCACTAGGAGG 2233
 QY 1549 ArgTyrGluThrGlnValGlnThrArgLeuGlnThrSerLeuAlaAsnLeuHisGlnLys 1568
 Db 2234 CGCTATGAACCTCAGGTACAACTTCGACTTCAGACCTCCCTTGCACATTCATCAGAAA 2293
 QY 1569 SerSerGluIleGluLeuAlaValAspLeuProLysGluThrIleLeuGlnPheLeu 1588
 Db 2294 AGCAGTGAATTTGAAATTTCTGCTGTGATCTTACCCAAAGAAACAATATTACAGTTTTTA 2353
 QY 1589 SerLeuGluTrpAspAlaAspGlnAlaPheAsnThrThrValLysGlnLeuLeuSer 1608
 Db 2354 TCATTAGAGTGGATGCTGATGAACAGCATTTACACAACTGTGAAGCAGCTGTGTCTCA 2413
 QY 1609 ArgLeuProLysGlnArgTyrLeuLysLeuValCysAspGluIleTyrAsnIleLysVal 1628
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QY 1629 GluLysValSerValLeuPheLeuTyrSerTyrArgAspTyrTyrArgIleLeu 1648
 Db 2474 GAAAAAAGGTGTCTGTGCTATTTCGTACAGCTATAGAGATGACTTACTACAGAATCTTA 2533
 QY 1649 Phe 1649
 Db 2534 TTT 2536
 RESULT 4
 US-09-925-301-184
 ; Sequence 184, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA106
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 184
 ; LENGTH: 2200
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2096)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2140)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2157)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2181)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc feature
 ; LOCATION: (2184)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-925-301-184

Alignment Scores:
 pred. No.: 1,1e-289 Length: 2200
 Score: 3029.00 Matches: 599
 Percent Similarity: 99.67% Conservative: 0
 Best Local Similarity: 99.67% Mismatches: 2
 Query Match: 35.45% Indels: 0
 DB: 10 Gaps: 0

US-09-515-806A-2 (1-1649) x US-09-925-301-184 (1-2200)
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 Db 10 AGCGACATCTCAAGGGCAACTTCTCAATCCGTACAGCCAAAGATGCAGCAGCATGTGTGT 69
 QY 1069 GluThrIleArgIlePheLysArgHisGlyAlaValGlnLeuCysThrProLeuLeu 1088
 Db 70 GAAACCATCATCCGCATCTTTAAAGACATGAGCTTTCAGTTGTGTCTCCACTACTG 129
 QY 1089 LeuProArgAsnArgGlnIleTyrGluHisAsnGluAlaAlaLeuPheMetAspHisSer 1108
 Db 130 CTTCGCCAAACAGACAAATATATAGCAACACAGAGCTGCCCTTATTCTATGACCACAGC 189
 QY 1109 GlyMetLeuValMetLeuProPheAspLeuArgIleProPheAlaArgTyrValAlaArg 1128
 Db 190 GGGATGCTGTGTATGCTTCTCTTTGACCTGCGGATCCCTTTTCAAGATATGTGCAAGA 249
 QY 1129 AsnAsnIleLeuAsnLeuLysArgTyrCysIleGluArgValPheArgProArgLysLeu 1148

Db 250 AATAATATATTGAATTTAAACGATCTGATAGAACGTGTGTTTCAGCGCCGCAAGTTA 309
QY 1149 AspArgPheHisProLysGluLeuLeuGluCysAlaPheAspIleValThrSerThrThr 1168
Db 310 GATCGATTTCATCCCAAGAACTTCTGGAGTGTGCATTTGATATGTCATCTTACCACC 369
QY 1169 AsnSerPheLeuProThrAlaGluIleIleIleIleIleIleIleIleIleIleIle 1188
Db 370 AACAGCTTTCGCCCACTGCTGAATTTATCTACATCTATCTATGAATCATCTCAAGAGTTT 429
QY 1189 ProAlaLeuGlnGluArgAsnThrSerIleIleIleIleIleIleIleIleIleIle 1208
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QY 1229 AspAlaValThrGluLysLeuThrArgArgGluValGluAlaLysPheCysAsnLeuSer 1248
Db 550 GATGCTGTGACAGAGAGCTGACGAGAGAGAGTGAAGCTAAATTTTGAATCTGTCT 609
QY 1249 LeuSerSerAsnSerLeuCysArgLeuTyrlLysPheIleGluGlnLysGlyAspLeuGln 1268
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QY 1269 AspLeuMetProThrIleAsnSerLeuIleLysGlnLysThrGlyIleAlaGluLeuVal 1288
Db 670 GATCTTATGCAACAATAAATTCATTAATAAACAAGAAACAGGTATTGACAGTTGGTG 729
QY 1289 LysTyrlGlyLeuLysAspLeuGluValValGlyLeuLeuLysLysLeuGlyIleLys 1308
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QY 1309 LeuGlnValLeuIleAsnLeuGlyLeuValTyrlLysValGlnGlnHisAsnGlyIleIle 1328
Db 790 TTACAGCTCTGATCAATTTGGCTTGTGTTACAGGTGACAGAGCAATGGGAATCATC 849
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QY 1349 GlyGlyArgTyrlAspLeuLeuIleProGlnPheArgGlyProGlnAlaLeuGlyProVal 1368
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QY 1369 ProThrAlaIleGlyValSerIleAlaIleAspLysIleSerAlaAlaValLeuAsnMet 1388
Db 970 CCCACTGCCATGGGGTCAGCATAGCTATAGCAAGATATCTGCTGCTGCTCAACATG 1029
QY 1389 GluGluSerValThrIleSerSerCysAspLeuLeuValValSerValGlyGlnMetSer 1408
Db 1030 GAGGAATCTGTACAAATAGCTTGTGACTCTGCTGTTGTAAGTGTGTGTCAGATGCT 1089
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QY 1429 MetTyrlAspTrpSerGlnSerGlnGluLeuGlnGluTyrlCysArgHisGluIle 1448
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Db 1330 AAACCTGAGGACTAAAGTCACTGATGAAGGAATGGCAGAGAAAGCTTCCGATATCTTGA 1389
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Db 1690 CGCTGCCAANCAAGAGATACCTCAATTAGTCTGTGATGAAATTTATAACATCAAGTA 1749
QY 1629 GluLysLysValSerValLeuPheLeuTyrlSerTyrlArgAspAspTyrlArgIleLeu 1648
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QY 1649 Phe 1649
Db 1810 TTT 1812

RESULT 5

US-09-801-368-117
; Sequence 117, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 117
; LENGTH: 4980
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-117

Alignment Scores:

Pred. No.: 4,67e-112 Length: 4980
Score: 1242.00 Matches: 462
Percent Similarity: 43.09% Conservative: 302
Best Local Similarity: 26.08% Mismatches: 682

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 964 AATCGATTGTTGGTTATACGGGTGAGCGCATGGGAGAAATAATGCAACGTTTGTTCG 1023
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 1024 AATAATAGACTCTTGACAGAGTACTGTAACACTATCCATTGGGAGATTTGATCAATCT 1083
 394 SerGlyProIleProValHisGlnLeuArgArgTyrThrAlaGlnLeuLeuSerGlyLeu 413
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 469 -----AsnAlaLeuProTyrLysThrGlyLysLys 478
 1324 CCAAGTACATGATGATAGCCCTGAGTTGTGAAATTCNATAACGCC-AAACCTCAAGATT 1382
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 1383 AACTGATATTGGCAACTTGGTGTGTTTGTATCCAGATAAATCAGTGGATCTGAT- 1437
 498 yGluTyrProValThrIleProSerAspLeuProAlaAspPhe----- 512
 1438 -----ATAGTGATGAATTTGAAACCCCTCAAGAACTCTAGATTCAACAAGTAT 1487
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 1788 TTCGACTTTGAGAGATTTCCAGTTTAGCCAGTGTAGCCAGGGCCATTTGGACAAAGTTGTCAAGGC 1847
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 647 nileValArgTyrTyrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyTh 667

Db 1962 TTTTGGCTTACTATGCTGCTAGTGGTATGAGAA----- 1995
QY 667 rProProAspSerGlyProLeuAlaLysAspArgAlaAlaArgGlyGlnProAl 687
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QY 687 aSerAspThrAspGlyLeuAspSerValGluAlaAlaProProIleLeuSerSe 707
Db 1996 -----GACAGTATGAT-----GA 2009
QY 707 rSerValGlnTrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAlaThrGl 727
Db 2010 AAACGTTTTTGAATCACTGATGAGAAAGTGACTTGAGC----- 2049
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QY 747 n-----SerPheLeuProAlaSerAspSerGl 756
Db 2109 TAGAACAAATCAAGATTTGGATAATAGTAAGTGGGATTTTCATATCGGGTCA---GGATA 2165
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Db 3300 GTATCTCTTAAATAATCAAGTCTGATTTCTAAGCAATATAGTACGACACGTTTACCG 3359
QY 1144 gProArgLysLeuAspArg-----PheHisProLysGluLeuLeuGluCysAlaPheAs 1162
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Db 3540 TCATGCTGATATTTTGGAGGTGTTTTCACACTTTACAAATATTGATAAGCCCAAGGCC 3599
QY 1220 -----LeuSerGlnValTyrcysIleLeuTyrcysAspAlaValThrGluLy 1234
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QY 1274 eAsnSerLeuIleLysGlnLysThrGlyIleAlaGlnLeuValLysTyrcysGlyLysAs 1294
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QY 1294 pLeuGluValValGlyLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 1314
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Db 3873 TCCTTTGTAGTAACTAAATAGCGCTTTTTCACAAAGGAGGTATCATGTTTTCATGCGATTTA 3932

us-09-515-806a-2.rnpb

Thu Jun 12 14:34:05 2003

GENERAL INFORMATION:
 APPLICANT: Stolk, John A.
 APPLICANT: Xu, Jiangchun
 APPLICANT: Chenault, Ruth A.
 APPLICANT: Mesgher, Madelein Joy
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
 FILE REFERENCE: 210121.561
 CURRENT APPLICATION NUMBER: US/09/998.598
 NUMBER OF SEQ ID NOS: 2606
 SOFTWARE: Corixa Invention Disclosure Database
 SEQ ID NO: 753
 LENGTH: 519
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-998-598-753

1334 eilleLysArgArgGlnArgAlaValProGluLeuLeuAlaGlyArgTyrAspLeu 1354
 3933 TGACGATGATCTCACGT-----AATATGATAGCTGCTGGAGGAGGTATGACAC 3983
 1354 uleuileProGlnPheArgGlyProGlnAlaLeuGlyProValProThr-----AlaI 1372
 3984 TTGTATATCTCTTTTGGCAGACCATTCAGAAAAAGAGCAGCAATACTCTGAAGGCTGT 4043
 1372 eGlyValSerIleAlaIleAspLysIleSerAlaValLeuLeu----- 1387
 4044 AGGTTCAACTAGCTGGGAAACAATAATTCGGTATAGCCCAAACTATTTCAAACCTCGC 4103
 1388 -----MetGluGluSerValThr----- 1393
 4104 TTCTGGAATATAGATAAAGAGAAATAGGTTTGTGAAGATACAGCTGTGTGTTGAA 4163
 1394 -IleSerSerCysAspLeuValValSerValGlyGlnMetSerMetSerArg---Al 1412
 4164 GCCAGCAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4223
 1412 aileAsnLeuThrGlnLysLeuTrpThrAlaGlyIleThrAlaGlyIleMetTyrAspTr 1432
 4224 GGTACCAATACTGAATACATTTGTGGAAGCAAAACATTAAAGCGATATGTTAAGGATG 4283
 1432 pSerGlnSerGlnGluLeuGlnGluTyrCysArgHisHisGluIleThrTyrValAl 1452
 4284 TTCC---TCGGTGGATGATCTGTTACTGCGCTCAACAGGATGTTATAGACTGATTT 4340
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 4341 GCTGATT-----AAGCAACAAGCGTATCCACTAACCAATCAACAGAGAAATCAAGCC 4394
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 4395 ATTTAAATAATAAAATGACACTATGTTGACATAGATTTAGATCTTGTGAGTGT 4454
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 4455 AACCTGTGACCAACAAGAACTGTTAAATCTTTGATCAACGATAGTCTCACTTTGGG 4514
 1510 nAsnLeuLysGlySerPhe-----SerAsnAlaSerGlyLeuPheG 1524
 4515 CGATAAGCTGATGAATTTAAAGATGGGATGAAACAGCAGTCCGCTAGTCAAGA 4574
 1524 u-----IleHisGlyAlaThr-----ValProIleValse 1535
 4575 AGGTGACATAGATGATGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4634
 1535 rValLeuAlaProGluLysLeuSerAlaSerThrArgArgArg-----TyrGluThrG 1553
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 1553 nValGlnThrArgLeuGlnThrSerLeuAlaAsnLeuHisGlnLysSerSerGluIleG 1573
 4695 AGCCAGAAATCTTCGAATATGATATACAAATTTA-----TCCAATGACC 4742
 1573 uileLeuAlaValAspLeuProLysGluThrIleLeuGlnPheLeuSerLeu----- 1590
 4743 AATATCACTGTTGATGCTTAAAGATGAAACTTTAGAAATATCTCAATCTCTTT 4802
 1591 -----GluTrp-----AspAlaAspGluG 1597
 4803 GGCTCAGAGGAAGATGGCTGAGAAAGTTTTTGGTTCAGGTAATAACTGACTCTCTAG 4862
 1597 nAlaPheAsnThrThrValLysGlnLeuLeuSerArg 1609
 4863 AAGCTTTGCCACGAGCATTTTATAATAACCTCTCCAAA 4899

RESULT 6
 US-09-998-598-753
 ; Sequence 753, Application US/09998598
 ; Patent No. US20020150922A1

RESULT 7
 US-09-918-995-24436
 ; Sequence 24436, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756

Alignment Scores: 3.8e-77 Length: 519
 Pred. No.: 873.00 Matches: 171
 Score: 873.00 Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 10.22% Gaps: 0
 DB: 10

US-09-515-806A-2 (1-1649) x US-09-998-598-753 (1-519)

QY 1135 LysArgTyrCysIleGluArgValPheArgProArgLysLeuAspArgPheHieProLys 1154
 Db 2 AAACGATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 61
 QY 1155 GluLeuLeuGluCysAlaPheAspIleValThrSerThrThrAsnSerPheLeuProThr 1174
 Db 62 GAATCTCGAGTGTGCAATTCATATTTGCTTCTTACCACCAACAGCTTCTTCCCACT 121
 QY 1175 AlaGluIleIleTyrThrIleTyrGluIleIleGlnGluPheProAlaLeuGlnGluArg 1194
 Db 122 GCTGAATATATACACTATCTATGAATCATCAAGAGTTTCCAGCACTTCCAGGAAAGA 181
 QY 1195 AsnTyrSerIleTyrLeuAsnHisThrMetLeuLeuLysAlaIleLeuLeuHisCysGly 1214
 Db 182 AATACAGTATTTATTGTAACCATACATGTTATTGAAAGCAATCTCTTACACTGTGG 241
 QY 1215 IleProGluAspLysLeuSerGlnValTyrIleLeuTyrAspAlaValThrGluLys 1234
 Db 242 ATCCAGAGATATAAATCACTCACTCAAGTCTACATTTCTGTATGATGCTGTGACAGAGA 301
 QY 1235 LeuThrArgArgGluValGluAlaLysPheCysAsnLeuSerLeuSerSerAsnSerLeu 1254
 Db 302 CTGACGAGGAGAGAGTGAAGCTAAATTTGTAAATCTGCTTTGCTTCTTAATAGTCTG 361
 QY 1255 CysArgLeuTyrLysPheIleGluGlnLysGlyAspLeuGlnAspLeuMetProThrIle 1274
 Db 362 TGTGACTCTCAAGATTTATTGAACAGAGAGGAGATTTCAGATCTTATGCAACAATA 421
 QY 1275 AsnSerLeuIleLysGlnLysThrGlyIleAlaGlnLeuValLysTyrGlyLeuLysAsp 1294
 Db 422 AATTCATTTAATAACACAGAAACAGGATTTGCAAGTTGGTGAAGTATGCTTTAAAGAC 481
 QY 1295 LeuGluGluValValGlyLeuLeuLysLysLeu 1305
 Db 482 CTAGAGGAGGTTGTTGGACTCTTGAAGAAACTC 514

22 1103 IGHIATAAAGTITCCGTTGCTGATTGGAAGGTCAATGGCGTTTAGTAGGAAGGAGGCCGCC 1164

Thu Jun 12 14:34:05 2003

QY	389	-----AlaHisLeuSerHisSerGly-	395	657	luArgHisGluArgProAlaGlyProGlyThrProPro-	669
Db	1165	TGGAATGGGAGTACCAGTTTGTACTCCCATCGGCTCGCTGGTGGTGGGATGGCA	1224	2158	AA-----ACCCACACAGAAAGTGGCAAGAGAGATGG	2190
QY	396	-----ProIleProValHisGlnLeuArgArgGlyThrAlaGlnLeuSerGlyL	413	670	-----ProAspSerGlyProLeuAlaLysEA	678
Db	1225	AGTCAATCCCATCAGCTGTTTGTATGATACAAAGTTACACAGCCAGC-----	1271	2191	ATGAGATCTGGCTCAAGACGAAAGACACAGACTGGCGCTCTCAGCTCCCTAGCCGATGG	2250
QY	413	euAspTyrLeuHisSerAsnSerValValHisLysValLeuSerAlaSerAsnValLeuV	433	678	spAspA:gaAlaAArgGlyGlnProAlaSerAspThrAspGlyLeuAspSerValGluA	698
Db	1272	-----GAAGAAGCCCTTGGAGACGAAAGACATTC	1302	2251	ATGCCCATCTGTTAAGATCCGAAGAGTGGATCTCTCCCTGGAGTTCTCTACAAAGAGACAGATCGAAG	2310
QY	433	alAspAla-----GluGlyThrValLysIleThrAspTyrSerIleSerL	448	698	laAlaAlaProProIleLeuSerSerSerVal-----GluT	711
Db	1303	TAGAGGCTGCTCGGGGAGCCACAGAGACAGCGTGTACTTTAGGATGTAC-----	1352	2311	TCATAGCTCTCTCTCTCGAAGAAAGTCCGCTCTTCTCGTGGGCATTTCTGTGGGCAGA	2370
QY	448	ysArgLeuAlaAspIleCysLysGluAspValPheGluGlnThrArgValArgPheSer-	467	711	tpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAlaThrGlyProGlySerS	731
Db	1353	-----AGAGGCCAGCTGTACCTGCAGTCGTCCGTCCGTCAGGGTCTCAG	1392	2371	CAAGCTCATCGAGAGCCAGTTCTCTCCCTGGAGTTCTCAGGACAGACTGCGGAGACA	2430
QY	468	-----AspAsnAla-----	470	731	erAspAspGluAspAsp-----	736
Db	1393	AAAAATTCCTACAAAGCCCAAGCCCTGGAGTCTGTAAATGGCAAAATGCATATTTC	1452	2431	ACAGTCACTACGCGACCGCCTACACCTCCAGGACAGTTGCTGCGGACTGCGAGG	2490
QY	471	--LeuPro-TyrLysThrGlyLysLysGlyAspValTrpArgLeuGlyLeuLeu-	487	737	-----AspGluAspGluHisGlyGlyValPheSerGlnSerPheL	750
Db	1453	CTCTGCCGACGATCAATATGAGCCCTTAATCCATCTCTCTTAGGACTCTCTGTCTGG	1512	2491	ACGTGGAAGATGGCACCGCTGGACGCAATGACAGGGGACACTCTCTTTGAACCTTTGTCGT	2550
QY	488	-----LeuLeuSerLeuSerGlnGlyGlnGlyCysGlyGluTyrProValThrIlePro	505	750	euProAlaSer-----AspSerGluSerAspIlelePheAspA	763
Db	1513	TGCGTCTGATGATTTGACAAAT-----GTCTAAGTAATGATAGTATTCTCC	1560	2551	CGAAGCTTCTCTCTATACCCGCTCTAGGGAAGAAACGCTCTCTCCATAGTTGTTGAGG	2610
QY	506	-----SerAspLeuProAlaAspPheGlnAsp-----	519	763	snGlu-----AspGluAsnSerLysSerGlnAsnGln-	773
Db	1561	ACGAAGAATACAGTAATGGTGCATTTCAATCTCCAGTATCCATACGATACCGTTACT	1620	2611	ACTCTGCTGCGCAACGCGTCCAGTAAAGAGAGAGCCAGAGGGAACCGGCTGCATGATG	2670
QY	520	ValCysLeuAspAspLysGluArg-----	527	774	-----AspGluAspCysAsnGluLysAsnGlyCysHisG	785
Db	1621	ATCTGCCATCTACAAAGAGAAAGAAATAGCGGACGACGACATACAGTCAGGTTCC	1680	2671	GCAACCATTAATTAATAGTAACCTGATCTCAAGTGTCCAGCAGCAGGCTCTTTCTTCAG	2730
QY	528	TrpSer-ProGlnGlnLeuLeuLysHisSerPheIleAsnProGlnProLysMetProLe	547	785	lu-----	785
Db	1681	TGGACAGCCCCCCTACAGCAAGAACATCCCAAGAGGACCTTATCTCTCTGTCGACT	1740	2731	AAGCCACCACTTGTCTTACCTCCCTACCAGGCCAACCACTCTAAGCTTGGATTTCACCA	2790
QY	547	ValGluGlnSerProGluAspSerGlyGlyGlnAsp-----	562	786	-----SerGluProSerValThrThrGluAlaValHisT	797
Db	1741	GGTGAAGGAGATATTTCGGGACGATCTCTGTCATCGTAGCCACGACCTTATCTGTCG	1800	2791	AGAACCTGTGGGCCAGCTCCAGCCAGCTCTCCCAAGGTG-----T	2832
QY	562	uThrValIleProSerAsnArgLeuProSerAlaAla-PhePheSerGluThrGlnArgG	582	797	yrLeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAspGlnG	817
Db	1801	GCAGGCTTTTCCATCTCA---GCCCCACAGCAGCGGAGAGTCTGAAACTCAGTGCC	1857	2833	ATCTGTACATTTCAGATGCAGCTGTGCAGGAAGAGAACCTCAAGAGACTGGATGAACCGC	2892
QY	582	ln-----	582	817	lyLeuTyr-----ArgAspThrValArgLeuTyrArgLeuPheArgGluIleLeuA	834
Db	1858	AGACTGAAGTAATACGACTCGTGTAGTCCGATGTCTAGTACAAACAGCTGGAATGACA	1917	2893	GCTGAGCTTGGAGACCGGAGCAGCGGCTGTGCTGCACATCTCTCCAGATCGCAG	2952
QY	583	-----PheSerArgTyrPheIleGluPheGluLeuGlnLeuLeuG	597	834	spGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnI	854
Db	1918	TGAAGTACTCAGGATACGTATCCGATATCTTAACAGATTTTGGCCAATTTCAGTGCATG	1977	2953	AGGAGTGGATTCTGTGCACAGCAAGGACTCATGCACAGGACCTCAAGCCCTTCCAAAC	3012
QY	597	lyLysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysTyrA	617	854	lePheLeuAspSerAspHisValIleGlyAspPheGlyLeuAlaThrAspHisL	874
Db	1978	GTCGTGTGCTTGGGTGTCTTTGAAGCTAAACAAACAAAGTAGATGACTGCAATTACG	2037	3013	TATTCTTCAATGGATGATGTGGTCAAGGTGGGACTTTGGACTGGTGGT-----	3065
QY	617	laValLysArgIleProIleAsnProAlaSerArgGlnPheArgGlyLysGlyGluV	637	874	euAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuLysSerAsp	894
Db	2038	CTATCAAGAGGATCCCGCTCCCAACAGGAGGTGGCCAGCGGAGAGGTAAATCCCGGAG	2097	3066	-----CCTATGGACCAAGATGAAGAAGAGCAGACT-----GTTCTGACTCCAATGC	3111
QY	637	alThrLeuLeuSerArgLeuHisGlnAlaValIleValArgTyrTyrAsnAlaTrpIleG	657	894	roSer---GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu---	912
Db	2098	TTAAGCCCTTGGCTAAGCTGGACACCCAGGCATTTGTAGGTATTTTCAACGCTGGTGG	2157	3112	CAGCTTATGTCACGACACCGGACCAAGTAGGAGCCCAAGCTATACATAGCCAGGACAGA	3171
QY				912	alGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIleI	932

Db 3172 TTCATGGAAACAAAC-----TACTCCCAATAGTGGACATCTCTTTAGGCTTGA 3222
 QY 932 lePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuA 952
 Db 3223 TTTCTGTTGAATCTCTTAC---CCATTCAGACCCAGATGGAACGAGTCCGATTTAA 3279
 QY 952 snGlnLeuArgAspProThSerProLysPheProGluAspPheAspGlyGluHisA 972
 Db 3280 CTGATGTGAGA-----AATCTCAAGTTTCTCTACTGTTCACCTCAG---AAATATC 3327
 QY 972 laLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThra 992
 Db 3328 CCCAAGAGCATATGATGGTTCAAGACATGCTCTCCATCCCCAGGAGCGCTGAAG 3387
 QY 992 laThrGluLeuLysSer-----GluLeuLeuProProProGlnMetGluGluS 1009
 Db 3388 CCACAGACATCAATGAAATGCCATATTTGAGAACTTGAGTTTCCCGG-GAAACCGTT 3446
 QY 1009 erGluLeuHisGluValLeuHisThrLeuThrAsnValAspGlyLysAlaTyrArgT 1029
 Db 3447 CTGAGACAGCGTCCCGCTCCATGAGTTTCATCTGGAAC-----AAAACATTCCAGA 3497
 QY 1029 hrMetMetAlaGlnIlePheSerGln 1037
 Db 3498 CA-----GCCAGCTGCTCGTACAG 3517

RESULT 9

US-10-197-666A-101
 ; Sequence 101, Application US/10197666A
 ; Publication No. US2003092037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAHI KASEI KABUSIKI KAISYA
 ; TITLE OF INVENTION: Elkl phosphorylation related gene
 ; FILE REFERENCE: PH-1548US
 ; CURRENT APPLICATION NUMBER: US/10/197,666A
 ; PRIOR FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: JP 2001-218204
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: JP 2001-263450
 ; PRIOR FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: JP 2002-012176
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 60/305,884
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: US 60/316,304
 ; PRIOR FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: US 60/350,027
 ; PRIOR FILING DATE: 2002-01-23
 ; NUMBER OF SEQ ID NOS: 156
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 101
 ; LENGTH: 4391
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (72)..(1961)
 US-10-197-666A-101

Alignment Scores:
 Pred. No.: 1,47e-36 Length: 4391
 Score: 479.00 Matches: 290
 Percent Similarity: 36.52% Conservative: 142
 Best Local Similarity: 24.51% Mismatches: 392
 Query Match: 5.61% Indels: 361
 DB: 9 Gaps: 55

US-09-515-806A-2 (1-1649) x US-10-197-666A-101 (1-4391)

QY 550 GlnSerProGluAspSerGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
 Db 456 AGGTCTGCTAAAGAGAGAGAGTTCGTGAGGATCTTCTGAGGATATTTCTCTGATCCAGAA 515

QY 570 LeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu 589
 Db 516 ATCAGATCAAGGAAAGTAGCCTTTGGAAAGCACAACCT-----TCAGGTACTTAATGNA 569
 QY 590 PheGluGluLeuGlnLeuLeuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsn 609
 Db 570 TTTGAAGAACTTCCCATCTTAGGAAAGGTGATACGGAAGAGATATACAAGGTCCAGGAAT 629
 QY 610 LysLeuAspGlyCysCysTyrAlaValLysArgIlePheProIleAsnProAlaSerArgGln 629
 Db 630 AAATTAGATGGTCAGTATTATGCAATAAAAAAACTCTGATTAAAGGGTGCACCTAAACA 689
 QY 630 Phe---ArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisHisGluAsnIle 648
 Db 690 GTTTGTCATGAAGGTCTTACGGGAAGTGAAGGTGTCGGCAGGTCTTTCAGCACCCCAATATT 749
 QY 649 ValArgTyrTyrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyThrPro 668
 Db 750 GTTGGCTATCACACCGCTGGATAGAA---CATGTTTCATGTGATTCAGCCA-----797
 QY 669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla---687
 Db 798 -----CGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTG 833
 QY 688 -----SerAspThrAsp 691
 Db 834 GAAGTGTCTCCGACCAGGAAGAGCAGACAGCAATGCTGTTAAAAATGATGAAAGT 893
 QY 692 GlyLeuAspSerValGluAlaAlaProProProIleLeuSerSerVal---Glu 710
 Db 894 AGCAGCTATCCATATCTTTGTCGACCCCAAGAAAAAGAAAAACCTTTGAGAA 953
 QY 711 TrpSerThrGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
 Db 954 TCTGACACTGAAATCAGAAATCAAGTCCGTGAAGTACACACCAATTTAGTCATAAGA 1013
 QY 729 GlySerSerAspGluAspAspGluAspGluHisGlyValPheSerGlnSer 748
 Db 1014 GAATCTGTTGAATCTTGTGACCTCGAGCTCCAGAAAAATGGCTTGGCTGTTGCT 1073
 QY 749 PheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsnSer 768
 Db 1074 -----GCCAGTTCAATTGTGGAACAGCAGCTGCCACTCAGCGCTAAATTTCCACCTAGAG 1127
 QY 769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGlnPro 788
 Db 1128 GAGAGTTTCATCCACCGAAGAACTCTCCGAAGAAATGTCAACTTTTGGGTGAG---1184
 QY 789 SerValThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu 806
 Db 1185 -----ACAGAGGCACAGTACCACCTGATGCTGCACATCCAGATGCACTGTGTGAG 1235
 QY 807 LysSerThrLeu-----ArgAspThrIleAspGln 816
 Db 1236 CTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAGCGCGCGGAGTAGTGTGACGAG 1295
 QY 817 GlyLeu-----TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAsp 834
 Db 1296 TCTGCTGCTCTTATGTTATGGCAATGTTGCCAACAAAAATTTTCAAGAAATGGTAGAA 1355
 QY 835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854
 Db 1356 GGTGTGTTTACATACATAAATCGGAATTTGTCACCGAGATCTGAAGCCCAAGAAATATT 1415
 QY 855 PheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla---ThrAsp 872
 Db 1416 TTTCTTCATGCCCTGATCAGCAAGTAAATAATAGGAGCTTTGCTGCGCTCCACAGAC 1475
 QY 873 HisLeuAlaPheSerAlaAspSerLysGlnAspGlnThrGlyAspLeuIleLysSer 892
 Db 1476 ATCCTA-----CAGAGAACACAGACTGGACCAACAGAAACCGGAAGAGA 1520

QY	893	AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu---	911	Db	2433	AAACCTTCCTGCTGCTCTAAGATAAAAGCTCAACTCTTTAAACAGGTACAGTGTG---	2487
Db	1521	ACACCAACA---CAT---ACGTCACAGTGGGTACTGTCTGTAGCTTCACCCGAACAG	1574	QY	1186	nGluPhePro-----AlaLeuGlnGluArgAsnTyrSerIleTyrLeuAsnHi	1202
QY	912	ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle	931	Db	2488	-CAACTTCCAACCTTTTATCTGTCTCTCCACCTTCAGTTAGTCGTCATCCAAACCA	2546
Db	1575	TTGGAAGA-----TCTGAGTATGATGCCAAGTCAGATATACAGCTTCGGGTG	1625	QY	1202	sThrMet-----LeuLeu	1206
QY	932	IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu	951	Db	2547	CACCTTGCAGAAAGCTTTGTACTCCGACCCACAGATGATCTCCAGGCAGCTCAGATCTCTT	2606
Db	1626	GTCTGCTAGAGCTC---TTTCACCCCTTTTGGAAACAGAAATGAGCGGACGACGATCTTA	1682	QY	1206	uLysAlaIleLeuLeuHisCysGlyIleProGluAspLysLeuSerGlnValTyrIleI	1226
QY	952	AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspGlyGluHis	971	Db	2607	TCCTGCTCTTTGCCCTCGCACTGT-----	2628
Db	1683	ACAGGTTTAAAG-----ACTGGTCAGTTCGGGAATCCCTCCGTAAA---AGGTGT	1730	QY	1226	eLeuTyrAspAlaValThrGluLysLeuThrArgGluValGluAlaLysPheCysAs	1246
QY	972	AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr	991	Db	2629	-----TCCCGGTACTCTCTCTTTATGTAGCACTCAGCTCCCAAGCAATCTGTAC	2681
Db	1731	CCAGTCAAGCAAGATATATACGACCTTAACGAGAAAGAACTCATCGCAGAGACCATCT	1790	QY	1246	nLeuSerLeuSerSerAsnSerLeuCysArgLeuTyrLysPheIleGluGlnLysGlyAs	1266
QY	992	AlaThrGluLeuLeuSerGluLeu-----	1000	Db	2682	A---TCCCTCAGAGCGCAGCATCTGAT-GAAATTTGGTT-----TTTGAATCCAGAAAGGTC	2734
Db	1791	GCCATTGAGCTGTCGAGAGTGAATCTTTCCAAATTTCTGAAATGTTAACTCACCCCTA	1850	QY	1266	pLeu-----	1270
QY	1001	-----LeuProProProGluMetGluGluSerGluLeuHisGluValLeuHis	1017	Db	2735	TCGCATGGAGTTGGCAGTCATCAGCGTAGATGCGGTATGATTTTGTGAATTTTAAATAA	2794
Db	1851	CAGATGAAGATAATAGCAAGAAAGAAATTCAGAACTTAAAGAGCAGCTAAACCTC	1910	QY	1271	-MetProThrIleAsnSerLeu-----	1277
QY	1018	ThrLeuThrAsnVal-----AspGlyLys-----	1025	Db	2795	AATGAACCAACATAAATACATGATGCTTTTATTGACACTTGACACTGGCCTAAATAAA	2854
Db	1911	CTTTCTCAAGACAAAGGGTGAGGATGACGGAAGGATGGGGCGTGGATGAAAGTGG	1970	QY	1278	-----	1278
QY	1026	-----AlaTyr-ArgThrMetMe	1031	Db	2855	AGACTCTGACTCTAATACAGTCCCTTACTGATAATAGCATGAAAGACCACTTCTT	2914
Db	1971	ACTTAACTTTAAGTAGTTAACTGGAATGTAATTTTAAATCTTTATATAGGGTATAGTT	2030	QY	1278	eLysGlnLysThrGlyIleAlaGlnLeuValLysTyrGlyLeuLysAspLeuGluVal	1298
QY	1031	tAlaGlnIlePheSerGlnArgIleSerProAlaIleAspTyrThrTyrAspSerAsp--	1050	Db	2915	AAAATCTAAA-----CCCTTTAAATACAGTACGGC-----	3077
Db	2031	GGTACATGCTCTGTTGATTTAGTAGCTTTTACAGACTTGTTTAAAGATGTCCAGAGTG	2090	QY	1298	lValGlyLeuLeuLysLys-----	1306
QY	1051	-----IleLeuLysGlyAsnPheSerIle	1058	Db	2963	TGAGGGCCGTGTTTAAAGAGCCAGGCTTTTCAAGACCTCATCCACCTCTGCACATGG	3022
Db	2091	CCCCAAGTCGCTTCT	2150	QY	1306	yLysLysLeuGlnValLeuIleAsnLeuGlyLeuValTyrLysValGlnGlnHisAsnG	1326
QY	1058	eArg-----ThrAlaLysMetGlnGlnHisValCysGluThrIleI	1072	Db	3023	CTGGCACTGTCACACTGCAGCTCCGCTCTGCTGAGGTACAGCACAGCACCAC	3077
Db	2151	TAAATATTAAACATATGCTAGTCTCTGAAACTTAAAACTTGGACCTCATCTCAATTAT	2210	QY	1326	yLysLysLeuGlnValLeuIleAsnLeuGlyLeuValTyrLysValGlnGlnHisAsnG	1346
QY	1072	eArgIlePheLysArgHisGlyAlaValGlnLeuCysThrProLeuLeuLeuProArgAs	1092	Db	3078	-----GTCTGCTGAGGTAGTTTCAATCCCGAGCGCAAGGGCTCTTCCCAAGAGCAG	3130
Db	2211	TTTCTCTTT-----CAACTCTGTTGACCTCTGCTGCTGCTCTCTCTCTCTCTCT	2252	QY	1346	uAlaAlaGlyGly-Arg-----TyrAspLeuLeuIleProGlnPheArgGlyProG	1363
QY	1092	nArgGlnIleTyrGluHisAsnGluAlaAlaLeuPheMetAspHisSerGlyMetLeuVa	1112	Db	3131	AGTTTCATGGAGCGGAAACACAGCGCTTTTCTTACTGCTCTCTCTCTCTCTCTCTCT	3190
Db	2253	TAGAAGTCTTACCCGCAAAATTTGATG-----	2280	QY	1363	lnAlaLeuGlyProValProThrAlaIleGlyValSerIleAlaIleAspLysIle-Ser	1382
QY	1112	lMetLeuProPheAspLeuArgIleProPheAlaArgTyrValAlaArgAsnIleIle	1132	Db	3191	TCGCA-----ATATCTACCCAGCTATCTATAAGGTTTCGCTTCGCGCATTAATGCT	3241
Db	2281	-GTGCTCCCT-----GCCTCTGCTCACTGCCCA-----	2307	QY	1383	AlaAlaValLeuAsnMetGluGluSerValThrIleSerSerCysAspLeuLeuVal---	1401
QY	1132	uAsnLeuLysArgTyrCysIleGluArgValPheArgProArgLysLeuAspArgPheHi	1152	Db	3242	TCTGCCCAACAGAGAGAACAGAAACGTCG-----CAATGTTCTCTTCGCTTCGA	3292
Db	2308	-----GCCCGGCTGCACATCTCA-----	2328	QY	1402	-----ValSerValGlyGlnMetSerMetSerMetSerMetSerMetSerMetSerMet	1419
QY	1152	sProLysGluLeuGluCys---AlaPheAspIleValThrSerThrThrAsnSerPh	1171	Db	3293	TGGGGCAGCATCGCTCGGATGCTGAAATTCATCTCCCTTCGCGCATTAATAAGAAAC	3352
Db	2329	-----CTGACTGTTCCAGTTTGGACAGCTGCCAGTCTCTCTCTCTCTCTCTCTCT	2372	QY	1420	TrpThrAlaGlyIleThr-----AlaGluIleMetTyrAspTrpSerGlnSer	1435
QY	1171	eLeuProThrAlaGluIleIleTyr-----	1179	Db	3353	ACCCAGGTAGCATCACCCAGAGCAGCCCTCGAGGAAAGTACTCGACAGTGGGGAAGGGA	3412

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Db      3413 CAGTCACC-----AAACACCACAGATGATGATCATGTGGAAAGGGTGT 3456
Qy      1456 AspLysGluGlySerHisValLysValLysSerPheGluLysGluArgGlnThrGluLys 1475
Db      3457 TCAAGAGAAACATCAT-----TTTCAGTCTGTCTCTAAGATGCTTACTACTGAAAG 3510
Qy      1476 ArgVal-LeuGluThrGluLeu-----1482
Db      3511 GGTTTAAGTGAACACTATGTATAAAAGTAACCAAGAGTCATCTCGTATTGATAT 3570
Qy      1483 -----ValAspHisValLeuGlnLysLeuArgThrLysVa 1494
Db      3571 GACACTTCTGAGCTAGAGGAGCCTCAGACCACCTGCTCCAATCCCTGCTGCTAAGGT 3630
Qy      1494 1 1494
Db      3631 T 3631

RESULT 10
US-10-198-846-12737/c
; Sequence 12737, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 12737
; LENGTH: 4448
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-12737

Alignment Scores:
Pred. No.: 2,97e-36 Length: 4448
Score: 476.00 Matches: 291
Percent Similarity: 36.69% Conservative: 143
Best Local Similarity: 24.60% Mismatches: 390
Query Match: 5.57% Indels: 361
DB: 9 Gaps: 56

US-09-515-806A-2 (1-1649) x US-10-198-846-12737 (1-4448)
Qy      550 GlnSerProGluAspSerGlyGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
Db      3928 AGGCTCTTAAGAGAGAGTTCCTCAGGATCCTGTGAGGATATTTCTCGTATCCAGAA 3869
Qy      570 LeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu 589
Db      3868 ATCAGATCAAGGGAAGTAGCTTGGAGACACAACT-----TCAGTACTTAATGAA 3815
Qy      590 PheGluGluLeuGlnLeuLeuGlyGlyGlyAlaPheGlyAlaValIleLysValGlnAsn 609
Db      3814 TTTGAGAACTTCCATCTTAGAAAGGTGATACGGAAGATATACAGGTCAAGT 3755
Qy      610 LysLeuAspGlyCysCysTyrAlaValLysArgIleProIleAsnProAlaSerArgGln 629
Db      3754 AAATTAGATGCTCAGTATTATCAATAAAAAAATCCCTGATTAGGGTGCACACTAATAACA 3695
Qy      630 Phe--ArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisHisGluAsnIle 648
Db      3694 GTTTCATGAGGTCCTACGGGAGTGAAGTGTGGCAGGTCTTCAGCACCCCATATT 3635

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Qy      649 ValArgTyrTyrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyThrPro 668
Db      3634 GTTGGCTATCACACCGGTGGATAGAA---CATGTTTCATGTGATTCAGCCA-----3587
Qy      669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla---687
Db      3586 -----CGAGCAGACAGAGTGCCTATTGAGTTGCCATCTCTG 3551
Qy      688 -----SerAspThrAsp 691
Db      3550 GAAGTCTCTCCGACCAGAGGACAGAGCAATGTGGTGTATAAAATGATGAAGT 3491
Qy      692 GlyLeuAspSerValGluAlaAlaProProProIleLeuSerSerVal---Glu 710
Db      3490 AGCAGCTCATCTATTCTTCTGAGCCACCCAGAAAAGAAAACGCTTTGGAGAA 3431
Qy      711 TrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
Db      3430 TCTGACACTGAAAAATCAGAATAACAAGTCGGTGAAGTACACCACCAATTTAGTCATAAGA 3371
Qy      729 GlySerSerAspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSer 748
Db      3370 GAATCTGTGAACTTGAGTCCACCTGGAGCTCCAGGAAAATGCTTGGCTGTTGCTCT 3311
Qy      749 PheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsnSer 768
Db      3310 -----GCCAGTTCAATTTGTGAAACAGCAGCTGCCACTCAGCGCTAATTTCCACCTAGAG 3257
Qy      769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluPro 788
Db      3256 GAGAGTTTCACATCCACCGAAGAATCTCCGAGAAAATGTCAACTTTTGGGTCAG---3200
Qy      789 SerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu 806
Db      3199 -----ACAGAGGCACAGTACCCTGATGCTGCACATCCAGATGCGCTGTGTGAG 3149
Qy      807 LysSerThrLeu-----ArgAspThrIleAspGln 816
Db      3148 CTCTCGCTGTGGATTGGATAGTCGAGAGAAACAAGCGCGCGGAGTATGTGGACGAG 3089
Qy      817 GlyLeu-----TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAsp 834
Db      3088 TCTGCCTGTCTCTTATGTTATGGCAATGTTCGACAAAATTTTCAAGATTTGTAGAA 3029
Qy      835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854
Db      3028 GGTGTGTTTACATACATAACATGGGAATGTGACCGAGATCTCAAGCCCAAGAAATATT 2969
Qy      855 PheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla---ThrAsp 872
Db      2968 TTTCTTCATGGCCCTGATCAGCAAGTAAATAATAGAGACTTTTGGTCTGGCTGCACAGAC 2909
Qy      873 HisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer 892
Db      2908 ATCCCTA-----CAGAAGAACACAGACTGGACCAACAGAAAACGGGAAGAGA 2864
Qy      893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu---911
Db      2863 ACACCAACA---CAT---ACGTCCAGATGGGTACTTGTCTGTACGCTTACCCGGAACAG 2810
Qy      912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
Db      2809 TTGGGAAGA-----TCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTG 2759
Qy      932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
Db      2758 GTTCCTGTAGAGTCT---TTTCACCGCTTTGGAAACAGAAATGGAGCGAGCAGAGAAGTTCTA 2702
Qy      952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHis 971
Db      2701 ACAGGTTTAAAG-----ACTGGTCAGTTCGCGGAATCCCTCCGCTAAA---AGGTGT 2654
Qy      972 AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr 991

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RESULT 11

US-10-197-666A-105
 ; Sequence 105, Application US/10197666A
 ; Publication No. US20030092037A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAHI KASEI KABUSIKI KAISYA
 ; TITLE OF INVENTION: Eiki phosphorylation related gene
 ; FILE REFERENCE: PH-1548US
 ; CURRENT APPLICATION NUMBER: US/10/197,666A
 ; PRIOR FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: JP 2001-218204
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: JP 2001-263450
 ; PRIOR FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: JP 2002-012176
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 60/305,884
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: US 60/316,304
 ; PRIOR FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: US 60/350,027
 ; PRIOR FILING DATE: 2002-01-23
 ; NUMBER OF SEQ ID NOS: 156
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 105
 ; LENGTH: 2776
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (90)..(1946)
 US-10-197-666A-105

Alignment Scores:
 Pred. No.: 4,728-36 Length: 2776
 Score: 470.50 Matches: 164
 Percent Similarity: 46.58% Conservative: 74
 Best Local Similarity: 32.09% Mismatches: 189
 Query Match: 5.51% Indels: 86
 DB: 9 Gaps: 23

US-09-515-806A-2 (1-1649) x US-10-197-666A-105 (1-2776)

QY	548	ValGluGlnSerPro---GluAspSerGlyGlnAspTyrValGluThrValIlePro	566
DB	492	GTCCGTCAGGATCTCTGTCAGATAAT-----TCITACATGCAAAATC-----	536
QY	567	SerAsnArgLeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTyr	586
DB	537	-----AGATCCAGAGAGATAGCTTCGAGCAAAACG-----TCACGCTAC	578
QY	587	PheIleGluPheGluGluGlnLeuLeuGlyGlyAlaPheGlyAlaValIleLys	606
DB	579	TTAAATGAATTTGAAGAGCTTGCCATCTTAGGAAAGAGGATATGGAGAGTTTACAA	638
QY	607	ValGlnAsnLysLeuAspGlyCysTyrAlaValIleArgIleProIleAsnProAla	626
DB	639	GTCCGAAACAAATATAGATGTCAGCATTATGCAATTAAGAAATCCTGATTAGAGCGCA	698
QY	627	SerArg---GlnPheArgIleLysGlyGluValThrLeuLeuSerArgLeuHis	645
DB	699	ACTAAACACAGATTGTATGAAGGTGCTACGGGANGTGAAGGTTCTGGCAGGTCTCCAGCAT	758
QY	646	GluAsnIleValArgTyrTyrAsnAlaTrpIleGluArg---HisGluArgProAlaGly	664
DB	759	CCCAATATTGTTGGTACCACACTCGTGGATAGAACATGTTTCATGTG-----	806
QY	665	ProGlyThrProProAspSerGlyProLeuAlaLysAspArgAlaAlaArgGly	684
DB	807	-----GTTCCACCCACAGACAGAGTTCGGAATCAACTGCCCTCTCTCGAAGTGTCTCG	860
QY	685	GlnProAlaSerAspThrAsp-----GlyLeuAspSerValGluAlaAla-----	700

DB	861	GAGCAGGAAGGGACAGACAGACCAGGTGGTTTAAAGATAATAAGAAAGAGTTCGTCCATT	920
QY	701	-----ProProIleLeuSerSerSerValGluTyr	711
DB	921	GTCTTTGCTGAACCTACCCAGAAAAAGAAACCTTTTGGGAGTCTGAGGTATAAAT	980
QY	712	SerThrSerGlyGluArgSerAlaSerAlaArgPheProAlaThrGlyProGlySerSer	731
DB	981	GAGAAATAACAACTGTGTGAGCTACAGCGCACTTAGTGGTCAGG-----AACAGCAGT	1034
QY	732	AspAspGluAspAspAspGluAspGluHisGlyGlyValPheSerGlnSerPheLeuPro	751
DB	1035	GAAGTGAATCGTCCATTGAGCTCCAGAGAGCGCTGACTGATTGCTCGTCAGACCA	1094
QY	752	AlaSerAspSerGluSerAspIleIlePheAspAsnGluAspGluAsnSerLysSerGln	771
DB	1095	GTTGTCAGGCATCAGCTCCGCTGGGCACTAGCTCGGAATTGGAAGGAAATTTTACATCC	1154
QY	772	AsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluProSerValThr	791
DB	1155	ACGGATGAGTCTTCTGAAGCAACTTGAACCTGCTGGGGCAGACGGAG-----	1202
QY	792	ThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGluLysSer	808
DB	1203	-----GTTCCGTACCACTGATGTTGCATCCAGATGCGAGTGTGTGAGCTCTCC	1253
QY	809	-----ThrLeuArgAspThrIleAspGlnGlyLeu	818
DB	1254	CTGTGGGACTGGATAACTGAGAGAAACAGCGGAGCGGAGTAGTGTGGACGAGGTCT	1313
QY	819	-----TyrArgAspThrValArgLeuTyrPheArgGluIleLeuAspGlyLeu	836
DB	1314	TGTCCTTATGTTATGGCCAGTGTGCAACAAATAATTTTCAAGATTGGTGGAGGTGC	1373
QY	837	AlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePheLeu	856
DB	1374	TTTTACATACATAACATGGGCATTTGCCAGAGATCTGAAGCCTAGAAATATTTTCTT	1433
QY	857	AspSer---AspAspHisValLysIleGlyAspPheGlyLeuAlaThrAspHisLeuAla	875
DB	1434	CATGGCCCTGATCAGCAAGTAAATAATAGGAGACTTTTGTCTGGCC-----	1478
QY	876	PheSerAlaAspSerLysGlnAspGlnThrGlyAspLeuIleLysSerAspProSer	895
DB	1479	---TGTCAGACATCATCCAGATG---CAGACTGGACCAACAGAAATGGGAAAGCAAC	1533
QY	896	GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu---ValGlnGly	914
DB	1534	GGACACAC-ACATCCAGAGTGGGACTTGTCTCTACGCATCACCAGAAACACAGGAGGA	1592
QY	915	SerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIleIlePhePhe	934
DB	1593	-----TCCAGTACGATCCCAAGTCAGATGATGATAGCTTGGGTGTGATCCTGCTC	1643
QY	935	GluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeu	954
DB	1644	GAGCTC---TTTCAGCCATTCGGGACAAATGAGCGGGCAACAGCTCTTAACAGGCGTA	1700
QY	955	ArgAspProThrSerProLysPheProGluAspPheAspGlyGluHisAlaLysGln	974
DB	1701	AGG-----ACTGGTCGGATACCCGAATCCCTCAGTAAA---AGGTGTCCGGTCAA	1748
QY	975	LysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGlu	994
DB	1749	GCCAAAGTATATCCAGCTCTTAACCGGGAGGATGCGTCAAGAGACCATCTGCCCTTCAG	1808
QY	995	LeuLeuLysSerGluLeuLeuProProPro-----GlnMet---GlnMet---	1006
DB	1809	CTGTCGAGAGTGTGAGCTTTTCAACCAACTGGAAATGTTAATCTCACATTGCGAGATGA	1868
QY	1007	-----GluGluSerGluLeuHisGluVal	1014

us-09-515-806a-2.rnpb

Thu Jun 12 14:34:05 2003

Db 1869 ATAATAGAACAGAGAAATTTGAAGAACTA 1901

RESULT 12

US-09-799-875-18

; Sequence 18, Application US/09799875

; Patent No. US20020034780A1

; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel

; APPLICANT: Kapeller-Libermann, Rosana

; APPLICANT: Williamson, Mark

; TITLE OF INVENTION: No. US20020034780A1 Human Protein Kinases and Uses

; FILE OF INVENTION: Therefor

; FILE REFERENCE: 35800/209996

; CURRENT APPLICATION NUMBER: US/09/799, 875

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/182,059

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 09/659,287

; PRIOR FILING DATE: 2000-09-12

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 1887

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-799-875-18

Alignment Scores: 2.77e-36 Length: 1887
Pred. No.: 470.00 Matches: 161
Score: 47.03% Conservative: 69
Percent Similarity: 47.03% Mismatches: 185
Best Local Similarity: 32.92% Indels: 74
Query Match: 5.50% Gaps: 22
DB:

US-09-515-806A-2 (1-1649) x US-09-799-875-18 (1-1887)

QY 550 GlnSerProGluAaspSerGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
Db 385 AGGCTCTGTAAGAGAGAGATTCTGTCAGGATCTTGTGAGGATATTTCTCGTATCCAGAAA 444
QY 570 LeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu 589
Db 445 ATCAGATCAAGGAAGTAGCTTGAAGCACAACACT-----TCACGTACTTAAATGAA 498
QY 590 PheGluGluLeuGlnLeuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsn 609
Db 499 TTGAAGAACTTGCATCTTAGGAAAGGTGGATACGGAAGAGATATACAGGTGCAACAT 558
QY 610 LysLeuAspGlyCysCysTyrAlaValLysArgIleProIleAsnProAlaSerArgGln 629
Db 559 AAATTAGATGGTCAGTATTATGCAATAAATAAATCCTGATTAAAGGTGCAACATAAACA 618
QY 630 Phe---ArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisHisGluAsnIle 648
Db 619 GTTTGTCATGAGGTCTCTACGGGAAGTGAAGGTGCTGGCAGGTCTTCACACCCCAATATT 678
QY 649 ValArgTyrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyThrPro 669
Db 679 GTTGGCTATCACACCGGTGGATAGAA---CATGTTTCATGTTGATTCAGCCA----- 726
QY 669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla--- 687
Db 727 -----CGAGACAGAGCTGCCATTGAGTTGCTCTCTCTG 759
QY 688 -----SerAspThrAsp 691
Db 760 GAAGTGCTCTCCGACCAAGAGAGGACAGAGCAATGTTGTTTAAATAATGATGAAAGT 819
QY 692 GlyLeuAspSerValGluAlaAlaProProProIleLeuSerSerVal---Glu 710
Db 820 AGCAGCTCATCCATTATCTTTGCTGAGGCCACCCCAAGAAAAAGAAAAACGCTTTTGAGAA 879

QY 711 TrpSerThrSerGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
Db 880 TCTGACACTGAAATCAGAAATACAAAGTCGGTCAAGTACACACCAATTTAGCTATAAGA 939
QY 729 GlySerSerAspAspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSer 748
Db 940 GAATCTGGTGAATGAGTCCACCTGGAGCTCCAGGAAATGGCTTGCTGGTTGCT 999
QY 749 PheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsnSer 768
Db 1000 -----GCCAGTTTCAATTTGGAAACACACCTCCACTCAGCGGTAAATCCCACTAGAG 1053
QY 769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluPro 788
Db 1054 GAGAGTTTCACATCCACCGAAGAAATCTTCGAAAGAAATCAACTTTTGGGTTCAG--- 1110
QY 789 SerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu 806
Db 1111 -----ACAGAGGCCACGTACCACTGATGCTGCATCCAGATGCAGATGCTGTGAG 1161
QY 807 LysSerThrLeu-----ArgAspThrIleAspGln 816
Db 1162 CTCTCGTGTGGATTGGATAGTCGAGAGAAACAAGCGGGCGGGAGTATGTGGAGAG 1221
QY 817 GlyLeu-----TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAsp 834
Db 1222 TCTGCCTGTCCTTATGTTATGCGCAATGTTGCAACAAAAATTTTCAAGAAATGCTAGAA 1281
QY 835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854
Db 1282 GGTGTGTTTATACATATAACATGGAATTTGTGACCGAGATCTGAAGCCCAAGAAATATT 1341
QY 855 PheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla---ThrAsp 872
Db 1342 TTTCTTCATGGCCCTGATCAGCAAGTAAATAATAGAGACTTTTGTCTGCGCTGCACAGAC 1401
QY 873 HisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer 892
Db 1402 ATCTCA-----CAGAAAGAACACAGACTGGACCAACAGAAACGGGAAGAGA 1446
QY 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911
Db 1447 ACACCAACA---CAT---ACGTCCAGAGTGGGTACTTGTCTGTACGCTTCAACCCGAACAG 1500
QY 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
Db 1501 TTGAAGAA-----TCTGATGATGATGCAAGTCAGATATGTACAGCTTGGGTGTG 1551
QY 932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
Db 1552 GTCCTGCTAGAGCTC---TTTTCAGCCCTTTTGGAAACAGAAATGGAGCGAGCAGAGTTCTTA 1608
QY 952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHis 971
Db 1609 ACAGGTTTAAAGA-----ACTGTCAGTTCGCGGAATCCCTCCGTAAA---AGGTGT 1656
QY 972 AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr 991
Db 1657 CCGGTGCAAGCCACAGTATATCCAGCACTTAACGAGAAAGAACTATCCGAGAGCACTCT 1716
QY 992 AlaThrGluLeuLeuLysSerGluLeu 1000
Db 1717 GCATTCTGCTGCTGACAGTGAACCTT 1743

RESULT 13

US-10-197-666A-103

; Sequence 103, Application US/10197666A

; Publication No. US20030092037A1

; GENERAL INFORMATION:

; APPLICANT: ASAHU KASEI KABUSIKI KAISYA

; TITLE OF INVENTION: Elkl phosphorylation related gene

; FILE REFERENCE: PH-154805

; CURRENT APPLICATION NUMBER: US/10/197,666A

; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: JP 2001-218204
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: JP 2001-263450
 ; PRIOR FILING DATE: 2001-08-31
 ; PRIOR APPLICATION NUMBER: JP 2002-012176
 ; PRIOR FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: US 60/305,884
 ; PRIOR FILING DATE: 2001-07-18
 ; PRIOR APPLICATION NUMBER: US 60/316,304
 ; PRIOR FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: US 60/350,027
 ; PRIOR FILING DATE: 2002-01-23
 ; NUMBER OF SEQ ID NOS: 156
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 103
 ; LENGTH: 2844
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (52)..(1938)
 ; US-10-197-666A-103

Alignment Scores:
 Pred. No.: 5,51e-36 Length: 2844
 Score: 470.00 Matches: 161
 Percent Similarity: 47.03% Conservative: 69
 Best Local Similarity: 32.92% Mismatches: 185
 Query Match: 5.50% Indels: 74
 DB: 9 Gaps: 22

US-09-515-806A-2 (1-1649) X US-10-197-666A-103 (1-2844)

QY 550 GlnSerProGluAspSerGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
 Db 436 AGGTCCTCTAAAGAGAGAGAGTCTCAGGATCTCTGGAGATATTCCTGATCCAGAAA 495
 QY 570 LeuProSerAlaAlaPheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu 589
 Db 496 ATCAGATCAAGGAAGTACGCTTGAAGCACAACCT-----TCAGTTACTTAATAGAA 549
 QY 590 PheGluGluLeuGlnLeuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsn 609
 Db 550 TTGTAAGAACTTGCCATCTTAGAAGAGTGTGATCGGAGAGATATACAGGTCAGGAAT 609
 QY 610 LysLeuAspGlyCysCysTyrAlaValLysArgIleProIleAsnProAlaSerArgGln 629
 Db 610 AATATAGATGTCAGTATATATGCAATAAAAAATCCTGATTAGGGTGCACATAAACA 669
 QY 630 Phe---ArgArgIleLysGlyGluValThrLeuSerArgLeuHisGluAsnIle 648
 Db 670 GTTTCATCAAGGTCCTACGGAAGTGAAGTGTGCTGCGAGGTCCTCAGCACCCCAATAT 729
 QY 649 ValArgTyrTyrAsnAlaTyrIleGluArgHisGluArgProAlaGlyProGlyThrPro 668
 Db 730 GTTGCTATACACCGCGTGATAGAA---CATGTTTCAGTGTATTCAGCA--- 777
 QY 669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla--- 687
 Db 778 -----CGAGACAGAGCTGCCATTGATTCCTCATCTG 810
 QY 688 -----SerAspThrAsp 691
 Db 811 GAAGTGTCTCTCCAGCAGGAGCAGAGAGCAATGTGGTGTAAATATGATGAAAGT 870
 QY 692 GlyLeuAspSerValGluAlaAlaProProIleLeuSerSerVal---Glu 710
 Db 871 AGCAGCTCATCATATCTTCTGAGCCCAACCCAGAAAAGAAACCTTTGAGAA 930
 QY 711 TrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
 Db 931 TCTGACACTGAATAATACAAAGTCTGCTGAGTGAAGTACACCACTTTAGTCATAAGA 990

QY 729 GlySerSerAspAspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSer 748
 Db 991 GAATCTGTGTAACCTTGAGTCAGCCCTGGAGCTCAGGAAAAATGCTTGGCTGGTTGTCT 1050
 QY 749 PheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsnSer 768
 Db 1051 -----GCCAGTTCAATTGTGGAACAGCAGCTGCCACTCAGCGCTAATTTCCACCTAGAG 1104
 QY 769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluPro 788
 Db 1105 GAGATTTTACATCCACCGAAGAAATCTTCGAAGAAAAATGTCACTTTTGGGTGAG--- 1161
 QY 789 SerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu 806
 Db 1162 -----ACAGAGGCACAGTACCACCTGATGCTGCACATCCAGATGCACTGTGTGAG 1212
 QY 807 LysSerThrLeu-----ArgAspThrIleAspGln 816
 Db 1213 CTCTGCTGTGGATTTGATAGTCGAGAGAAACAGCGGGCGGAGTATGTGACGAG 1272
 QY 817 GlyLeu-----TyrArgAspThrValArgLeuTyrPargLeuPheArgGluIleLeuAsp 834
 Db 1273 TCTGCTGTGCTTATGTTATGTCACAAAAATTTTCAAGAAATTTGGTAGAA 1332
 QY 835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854
 Db 1333 GGTGTGTTTACATACATACATGGAATTTGTGCGCAGATCTGAAGCAAGAAATATT 1392
 QY 855 PheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla---ThrAsp 872
 Db 1393 TTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGAGACTTTGGTCTGCGCTGCACAGAC 1452
 QY 873 HisLeuAlaPheSerAlaAspSerLysGlnAspGlnThrGlyAspLeuIleLysSer 892
 Db 1453 ATCCTA-----CAGAAGAACACAGACTGCACCAACAGAAACGGGAAGAGA 1497
 QY 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911
 Db 1498 ACACCAACA---CAT---ACGTCAGAGTGGGTACTTCTGTCTAGCTTACCCGGAACAG 1551
 QY 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
 Db 1552 TTGGAAGGA-----TCTGAGTATGATGCCAAGTCAGATATGATACAGCTTGGGTGTG 1602
 QY 932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
 Db 1603 GTCTGCTAGAGCTC---TTTCAGCCGTTTGGAAACAGAAATGGAGCGAGCAGAAAGTTCTA 1659
 QY 952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGlyGluHis 971
 Db 1660 ACAGGTTTAAAG-----ACTGTCAGTTCGCGGAATCCCTCCGTAAA---AGTGT 1707
 QY 972 AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr 991
 Db 1708 CCAGTGCAGCAAGTATATATCCAGCACTTAACGAGAAGNACTCATTCGAGAGACCATCT 1767
 QY 992 AlaThrGluLeuLeuLysSerGluLeu 1000
 Db 1768 GCCATTGCTGTGACAGTGAACCTT 1794

RESULT 14

; US-09-799-875-16
 ; Sequence 16 Application US/09799875
 ; Patent No. US20020034780A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel
 ; APPLICANT: Kapeller-Libermann, Rosana
 ; APPLICANT: Williamson, Mark
 ; TITLE OF INVENTION: No. US20020034780A1el Human Protein Kinases and Uses
 ; FILE REFERENCE: 35800/205996
 ; CURRENT APPLICATION NUMBER: US/09/799,875

769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluPro 788
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1167 GAGAGTTTTCATCCACCGAAGAATCTTCCGAAGAAATGTCAACTTTTGGTGAC--- 1223

Db

789 SerValThrThrGluAlaValHistyr-----LeuTyrIleGlnMetGluTyrCysGlu 806
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1224 -----ACAGAGGCACAGTACCACCTGCTGCACATCCAGATGCGCTGTGTGAG 1274

Db

807 LysSerThrLeu-----ArgAspThrIleAspGln 816
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1275 CTCTCGCTGTGGGATTGGATGTCGAGAGAAAACAAGCGGGCGGAGTATGTGCACGAG 1334

Db

817 GlyLeu-----TyrArgAspThrValArgLeuTyrPargLeuPheArgGluIleLeuAsp 834
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1335 TCTGCTGTCCTTATGTTATGCCAATGTTGCCAACAAAAATTTTTCAAGAAITGGTAGAA 1394

Db

835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1395 GGTTGCTTTTACATACATAACATGGGAATTGTGCACCGAGATCTGAAGCCAGAGAAATATT 1454

Db

855 PheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla---ThrAsp 872
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1455 TTCTTTCATGGCCCTGATCAGCAAGTAATAATAGAGACATTGGTCTGGCTGCACAGAC 1514

Db

873 HisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer 892
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1515 ATCCCTA-----CAGAAGAACACACAGACTGCACCAACAGAAACCGGACGAGAGA 1559

Db

893 AspProSerGlyHisIleThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1560 ACACCAACA---CAT---ACGTCACAGTGGGTACTTGTCTGTACGCTCACCCGAAACAG 1613

Db

912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1614 TTGGHAGA-----TCTGAGTAGATGCCAAGTCAGATATGTACGACTTGGGTGTG 1664

Db

932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1665 GTCCCTGCTAGAGCTC---TTTCACCCGTTTGGAACAGAAATGGACGACGACAGATTCCTA 1721

Db

952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspGlyGluHis 971
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1722 ACAGGTTTAAAG-----ACTGGTCAGTTGCCGGAATCCCCTCCGTAAA---AGGTGT 1769

Db

972 AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr 991
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1770 CCGGTGCACCCCAAGTATATCCAGCACTTAACGAGAAAGAACTCATCCGACAGACCATCT 1829

Db

992 AlathrGluLeuLeuLysSerGluLeu 1000
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1830 GCCATTCAAGCTGTGCAGAGTGAACCTT 1856

Db

RESULT 15
US-10-197-666A-107
; Sequence 107, Application US/10197666A
; Publication No. US20030092037A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISYA
; TITLE OF INVENTION: Etk1 phosphorylation related gene
; FILE REFERENCE: PH-1548US
; CURRENT APPLICATION NUMBER: US/10/197,666A
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: JP 2001-218204
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: JP 2001-263450
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: JP 2002-012176
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 60/305,884
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/316,304
; PRIOR FILING DATE: 2001-09-04

[illegible]

; PRIOR APPLICATION NUMBER: US 60/350,027
 ; PRIOR FILING DATE: 2002-01-23
 ; NUMBER OF SEQ ID NOS: 156
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 107
 ; LENGTH: 2768
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (213)..(2069)
 ; US-10-197-666A-107

Alignment Scores:
 Pred. No.: 1,17e-35 Length: 2768
 Score: 466.50
 Percent Similarity: 44.97%
 Best Local Similarity: 30.20%
 Query Match: 5.46%
 DB: 99
 Gaps: 27

US-09-515-806A-2 (1-1649) x US-10-197-666A-107 (1-2768)

QY 472 ProTyrIysThrGlyLysLysGlyAspValTTPArgLeuGlyLeuLeuLeuSerLeu 491
 DB 370 CCCTACAGCAGCCACGCTCCCTTCCTGCTGCGAACCAG-CTGCTGCTGCTCCTTA 428
 QY 492 SerGlnGlyGlnGluCysGlyGluTyrProValThrIleProSerAspLeuProAlaAsp 511
 DB 429 CTGGAACACTTGAGCCATGTGCAGCAGCCAAACCGCTCCACTCCAAACAGGTGTTAAA 488
 QY 512 Phe-----GlnAspPheLeuLys-----LysCysValCysLeuAspAsp 524
 DB 489 TTACTGTGCGACACTTTTATCAAGATGGGCTGCTCTCTCTTACCTGCGAGTGATGAG 548
 QY 525 -----LysGluArgTyrSerProGlnGlnLeuLeuLysHisSerPheIleAsnProGln 542
 DB 549 TTTACTCTCTGAGACTCCACCAACAGAGCCCACTCATTTAATGAGGTCTGCCAA 608
 QY 543 ProLysMetProLeuValGluGlnSerPro---GluAspSerGlyGlyGlnAspTyrVal 561
 DB 609 CAGAGA-----GTCCGTGAGATCCTTGTCAAGATAAT-----TCTTACATG 650
 QY 562 GluThrValIleProSerAsnArgLeuProSerAlaAlaPhePheSerGluThrGlnArg 581
 DB 651 CAGAAATC-----AGATCCAGAGAGATAGCCCTTCGAAGCAAAACG----- 692
 QY 582 GlnPheSerArgTyrPheIleGluPheGluGluGlnLeuLeuGlyLysGlyAlaPhe 601
 DB 693 -----TCACGCTACTTAATGAATTTGAAGAGCTTGCCATATGCAATTAAGAAATC 746
 QY 602 GlyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAlaValLysArgile 621
 DB 747 GGAAGAGTTTACAGGTCCGGAACAAATTAGATGGTCACCATATGCAATTAAGAAATC 806
 QY 622 ProIleAsnProAlaSerArg---GlnPheArgArgIleLysGlyGluValThrLeu 640
 DB 807 CTGATTAAAGAGCCCACTAAACAGATTGTATGAAGGTGCTACGGGAAGTGAAGTCTTG 866
 QY 641 SerArgLeuHisGluAsnIleValArgTyrTyrAsnAlaTTPileGluArg---His 659
 DB 867 GCAGGTCTCCAGCATCCCAATATTTGGCTACCACTGCTGGTGAATGAACATGTTTCAT 926
 QY 660 GluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLysAspAsp 679
 DB 927 GTG-----GTTCCAGCCCAAGACAGAGTTCGATTCACATGCCCTCT 968
 QY 680 ArgAlaAlaArgGlyGlnProAlaSerAspThrAsp-----GlyLeuAspSerValGlu 697
 DB 969 CTCGAAGTCTCTCGGAGCAGGAGGGGACAGACCAAGGTGTGTTAAGATAATGA 1028
 QY 698 AlaAlaAla-----ProProIleLeuSer 706

DB 1029 AGCATTGCTGCATTTGCTGTGTAACCTCACCCAGAAAGAAACCTTTTGGGAG 1088
 QY 707 SerSerValGluThrPsrThrSerGlyGluArgSerAlaSerAlaArgPheProAlaThr 726
 DB 1089 TCTGAGGTTAAAAATAGAATAACAACCTGCTGCTACCGCCCACTTAGTGTGTCAG 1148
 QY 727 GlyProGlySerSerAspGluAspAspGluAspGluHisGlyGlyValPheSer 746
 DB 1149 -----AACAGCAGTGAAGTGAATCGTCCATTGAGCTCCAAGAGACGCTTACTGAT 1202
 QY 747 GlnSerPheLeuProAlaSerAspSerGluSerAspIleIlePheAspAsnGluAspGlu 766
 DB 1203 TTGTCGCTCAGACCACTTGTTCAGGCATCAGCTCGCTGGGCATAGTTCGGAATTGAA 1262
 QY 767 AsnSerLysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSer 786
 DB 1263 GGGAAATTTTACATCCACGATCAGTCTTCTGAAGCAACTTGAACCTCTGCGGCAGACG 1322
 QY 787 GluProSerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGlu 803
 DB 1323 GAC-----GTTCCGTACCACTGATGTTGCCACATCCAGATCGAG 1361
 QY 804 TyrCysGluLysSer-----ThrLeuArgAspThr 813
 DB 1362 CTGTGTGAGCTCTCCCTCTGGGACTGGATAACTCAGAGGAACAAGCGGCGGAGTAT 1421
 QY 814 IleAspGlnGlyLeu-----TyrArgAspThrValArgLeuTyrArgLeuPheArgGlu 831
 DB 1422 GTGGACGAAGCTGCTGCTCCCTATGTTATGGCCAGTGTTCGCAACAAATTTTCAAGAA 1481
 QY 832 IleLeuAspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysPro 851
 DB 1482 TTGTGGAAAGTGTCTTTTACATACATAAATCGGCATGTCACAGAGATCTGAAGCCT 1541
 QY 852 ValAsnIlePheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAla 870
 DB 1542 AGAAATATTTTCTTCATGCTGCTGATCAGCAAGTAAAAATAGGAGACTTGTCTCTGCC 1601
 QY 871 ThrAspHisLeuAlaPheSerAlaAspSerLysGlnAspGlnThrGlyAspLeuLeu 890
 DB 1602 -----TGTGCAGACATCATCCAGATG--CAGACTGGACCAACAGAA 1641
 QY 891 LysSerAspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerPro 910
 DB 1642 ATGGAAAGAAACACCGACACAC-ACATCCAGAGTGGGACTTGTCTTACGCATCACCG 1700
 QY 911 Glu---ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeu 929
 DB 1701 GAACAGCTGGAGGA-----TCCAGTAGGATGCCAAGTCAGATATGTATAGCTTG 1751
 QY 930 GlyIleIlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgilePhe 949
 DB 1752 GGTGTGATCTCTCTGAGCTC---TTTCAGGCATTCGGGACAGAAATGGACAGGCAACA 1808
 QY 950 ValLeuAsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspAspGly 969
 DB 1809 GTCTTAACAGGCGTAAGG-----ACTGTCGGATACCCGAATCCCTCAGTAAA--- 1856
 QY 970 GluHisAlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArg 989
 DB 1857 AGGTCTCGGTGCAAGCCCAAGTATATCCAGCTCTAACCGGAGGAATGTGTACAGAGA 1916
 QY 990 ProThrAlaThrGluLeuLysSerGluLeuLeuProPro----- 1004
 DB 1917 CCATCTGCCCTTCAGCTGCTGCAGAGTGTGCTTTTCAACAACTGGAATGTTAATCTC 1976
 QY 1005 -----GlnMet-----GluGluSerGluLeuHisGluVal 1014
 DB 1977 ACATTGCAGATGAAGATAATAGAACCAAGAGAGAAATTAAGAACTA 2024

Search completed: June 12, 2003, 08:25:30
 Job time : 1084 secs

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Thu Jun 12 14:34:05 2003